



ATGTGGAAATGGATACTGACACATTGTGCCTCAGCCTTCCCCACCTGCCGGCTGCTGC  
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60  
TACACCTTACCTATGACTGTGTAACACGGAGTCGGAAAGGGGTGGACGGGCCGACGACG  
M W K W I L T H C A S A F P H L P G C C  
TGCTGCTGCTTTGTTGCTGTTCTGGTGTCTCCGTCCCTGTCACCTGCCAAGCCCTT  
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120  
ACGACGACGAAAAACAACGACAAGAACACAGAAGGCAGGGACAGTGGACGGTTGGAA  
C C C F L L L F L V S S V P V T C Q A L  
GGTCAGGACATGGTGTACCAAGAGGCCACCAACTCTTCTTCCCTCCTCTCCT  
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 180  
CCAGTCCTGTACCAACAGTGGTCTCCGGTGGTTGAGAAGAAGGAGGAGGAAGAGGAGGAGGA  
G Q D M V S P E A T N S S S S S S F S S P  
TCCAGCGCGGGAAAGGCATGTgCGGAGCTACAATCACCTCAAGGAGATGTCCGCTGGAGA  
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 240  
AGGTTCGCGCCCTTCCGTACACGCCTCGATGTTAGTGGAAAGTTCTACAGGCGACCTCT  
S S A G R H V R S Y N H L Q G D V R W R

MATCH WITH FIG. 1B

FIG.1A

MATCH WITH FIG. 1A

AAGCTATTCTCTTCAACCAAGTACTTCTCAAGATTGAGAAGAACGGGAAGGTAGCGGG  
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300  
TTCGATAAGAGAAAGTGGTCATGAAAGAGTTCTAACTCTTCTGCCCTCCAGTCGCC  
  
K L F S F T K Y F L K I E K N G K V S G  
  
ACCAAGAAGGAGAACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT  
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360  
TGGTTCTTCCTCTTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTAGCCTCAA  
  
T K K E N C P Y S I L E I T S V E I G V  
  
GTTGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGAAACTC  
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420  
CAACGGCAGTTCGGTATTGTCGTTGATAATGAATCGGTACTGTTCTCCCTTGAG  
  
V A V K A I N S N Y Y L A M N K K G K L  
  
TATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAATGGA  
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480  
ATACCGAGTTTCTTAAATTGTTACTGACATTGACTTCCTCTCCTATCTCCTTTACCT  
  
Y G S K E F N N D C K L K E R I E E N G

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

181 TACAATACCTATGCATCATTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540  
ATGTTATGGATACGTAGTAAATTGACCGTCGTATTACCCCTCCGTTACATACACCGTAAC  
Y N T Y A S F N W Q H N G R Q M Y V A L  
AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCAC  
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600  
TTACCTTTCTCGAGGTTCTCTCCTGTCTTGTGCTTCCTTTGTGGAGACGAGTG  
N G K G A P R R G Q K T R R K N T S A H  
TTTCTTCCAATGGTGGTACACTCATAG  
601 -----+-----+----- 627  
AAAGAAGGTTACCAACATGTGAGTATC  
F L P M V V H S \*

FIG. 1C

1

50

FGF4 MS.GPGTAAV ALLPAVLLAL LA..... .PWAGRGGAA APTAPNGTLE  
FGF6 MSRGAGRLQG TLWALVFLGI LV..... .GMVVPSAG TR.ANNTLLD  
FGF5 .....MSL SFLLLFFSH LILSAWAHGE KRLAPKGQPG PAATDRNPIG  
FGF1 .....  
FGF2 .....  
FGF9 ..... .MAPLGEVG NYFGVQDAVP  
FGF7 ..... .MHKW ILTWILPTLL ..... YRSCF HIICLVGTIS  
KGF2 ..... .MWKW ILTHCASAfp HLPGCCCCF LLLFLVSSVP  
FGF3 .....  
FGF8 MGSPRSALSC LLLHLLVLCL QAQVRSAAQK RGPGAGNPAD TLGQGHEDRP

51

100

FGF4 AELERRWESL VALSIARLPV AA..QPKEAA VQSGAGDY... .LLGIKRL  
FGF6 S...RGWGL LSRSRAGLAG EI.....AG VNWESG.Y... .LVGIKRQ  
FGF5 SSSRQSSSSA MSSSSASSSP AASLGSQGSG LEQSSFQW... .SPSGRRT  
FGF1 .....MAEG EITTFTALTE KFN...LPPG .....N...YK...KP  
FGF2 .....MAAG SITTLPALPE DGGSGAFPPG .....H...FK...DP  
FGF9 FGNVPVLPVD SPVLLSDHLG QSEAGGLPRG PAVTDLDH... .LKGILRR  
FGF7 LACNDMTPEQ M...ATNVNC .....SSPE RHTRSYDY... .MEGGDIR  
KGF2 VTCQALGQDM VSPEATNSSS SSFSSPSSAG RHVRSYNH... .LQ.GDVR  
FGF3 PGWPAAGPGA ..... RLRRDAG GRGGVYEH... .L.GGAPR  
FGF8 FGQRSRAGKN FTNPAPNYPE EGSKEQRDSV LPKVTQRHVR EQSLVTDQLS

MATCH WITH FIG. 2B

FIG. 2A

MATCH WITH FIG. 2A

	101	150
FGF4	RRL.....YC NVGIGFHLQA LPDGRIGGAH ADT.RDSLLE LSPVERGV.V	
FGF6	RRL.....YC NVGIGFHLQV LPDGRISGTH EEN.PYSLLE ISTVERGV.V	
FGF5	GSL.....YC RVGIGFHLQI YPDGKVNGSH EAN.MLSVLE IFAVSQGI.V	
FGF1	KLL.....YC SNG.GHFLRI LPDGTVDGTR DRSDQHIQLQ LSAESVGE.V	
FGF2	KRL.....YC KNG.GFFLRI HPDGRVDGVR EKSDPHIKLQ LQAEERGV.V	
FGF9	RQL.....YC R.T.GFHLEI FPNGTIQGTR KDHSRGFILE FISIAVGL.V	
FGF7	VRR.....LF CRT.QWYLRI DKRGKVKGQTQ EMKNYNIME IRTVAVGI.V	
KGF2	WRK.....LF SFT.KYFLKI EKNGKVSGTK KENCPYSILE ITSVEIGV.V	
FGF3	RRK.....LY CAT.KYHLQL HPSGRVNGSL .ENSAYSILE ITAVEVGI.V	
FGF8	RRLIRTYQLY SRTSGKHVQV LANKRINAMA EDGDPFAKLI VETDTFGSRV	

	151	200
FGF4	SIFGVASRFF VAMSSKGKLY G.SPFFTDEC TFKEILLPNN YNAYESYKYP	
FGF6	SLFGVRSALF VAMNSKGRLY A.TPSFQEEC KFRETLLPNN YNAYESDLYQ	
FGF5	GIRGVFSNKF LAMSKKGKLH A.SAKFTDDC KFRERFQENS YNTYASAIHR	
FGF1	YIKSTETGQY LAMDTDGLLY G.SQTPNEEC LFLERLEENH YNTYISKHH.	
FGF2	SIKGVCANRY LAMKEDGRLL A.SKCVTDEC FFFERLESNN YNTYRSRKY.	
FGF9	SIRGVDSGLY LGMNEKGELY G.SEKLTQEC VFREQFEENW YNTYSSNLYK	
FGF7	AIKGVESEFY LAMNKEGKLY A.KKECNEDC NFKELILENH YNTYAS....	
KGF2	AVKAINSNEY LAMNKKGKLY G.SKEFNNDC KLKERIEENG YNTYAS....	
FGF3	AIRGLFSGRY LAMNKRGRLY A.SEHYSAEC EFVERIHELG YNTYASRLYR	
FGF8	RVRGAETGLY ICMNKKGKLI AKSNGKGKDC VFTEIVLENN YTALQNAKY.	

MATCH WITH FIG. 2C

FIG. 2B

MATCH WITH FIG. 2B

	201	250
FGF4	.....	GM.....FI ALSKNGKTKK G..NRVSPTM KVTHFLPRL.
FGF6	.....	GT.....YI ALSKYGRVKR G..SKVSPIM TVTHFLPRI.
FGF5	.....	TEKTGREWYV ALNKRGKAKR GCSPRVKPQH IsthFLPRFK
FGF1	.....	...AEKNWFV GLKKNGSCKR G..PRTHYGQ KAILFLPLPV
FGF2	.....	...T..SWYV ALKRTGQYKL G..SKTGPQG KAILFLPMSA
FGF9	HV.....	..DTGRRYYV ALNKGDTPRE G..TRTKRHQ KFTHFLPRPV
FGF7	.....	AKW THNGGEM.FV ALNQKGIPVR G..KKTKEQ KTAHFLPMAI
KGF2	.....	FNW QHNGRQM.YV ALNGKGAPRR G..QKTRRKN TSAHFLPMVV
FGF3	TVSSTPGARR	QPSAERLWYV SVNGKGRPRR G..FKTRRTQ KSSLFLPRVL
FGF8	.....	....EGWYM AFTRKGRPRK G..SKTRQHQ REVHFMKRLP

	251	300
FGF4	.....	.....
FGF6	.....	.....
FGF5	QSEQPELSFT	VTVPEKKNPP SPIKSKIPLS APRKNTNSVK YRLKFRFG..
FGF1	SSD.....	.....
FGF2	KS.....	.....
FGF9	DPDKVPELYK	DILSQS.....
FGF7	T.....	.....
KGF2	HS.....	.....
FGF3	DHRDHEMVRQ	LQSQLPRPPG KGVQPRRRRQ KQSPDNLEPS HVQASRLGSQ
FGF8	RGHHTTEQSL	RFEFLNYPPF TRSLRGSQRT WAPEPR.....

MATCH WITH FIG. 2D

FIG. 2C

MATCH WITH FIG. 2C

301

FGF4	.....
FGF6	.....
FGF5	.....
FGF1	.....
FGF2	.....
FGF9	.....
FGF7	.....
KGF2	.....
FGF3	LEASAH
FGF8	.....

FIG.2D

GGAATTCCGG	GAAGAGAGGG	AAGAAAACAA	CGGCGACTGG	GCAGCTGCCT	CCACTTCTGA	60
CAACTCCAAA	GGGATATACT	TGTAGAAGTG	GCTCGCAGGC	TGGGGCTCCG	CAGAGAGAGA	120
CCAGAAGGTG	CCAACCGCAG	AGGGGTGCAG	ATATCTCCCC	CTATTCCCCA	CCCCACCTCC	180
CTTGGGTTTT	GTTCACCGTG	CTGTCATCTG	TTTTCAGAC	CTTTTGGCA	TCTAACATGG	240
TGAAGAAAGG	AGTAAAGAAG	AGAACAAAGT	AACTCCTGGG	GGAGCGAAGA	GCGCTGGTGA	300
CCAACACCAAC	CAACGCCACC	ACCAGCTCCT	GCTGCTGCAG	CCACCCACGT	CCACCATTAA	360
CCGGGAGGCT	CCAGAGGCAGT	AGGCAGCGGA	TCCGAGAAAG	GAGCGAGGGG	AGTCAGCCGG	420
CTTTCCGAG	GAGTTATGGA	TGTTGGTGCA	TTCACTTCTG	GCCAGATCCG	CGCCCAGAGG	480
GAGCTAACCA	GCAGCCACCA	CCTCGAGCTC	TCTCCTTGCC	TTGCATCGGG	TCTTACCCCTT	540
CCAGTATGTT	CCTTCTGATG	AGACAATTTC	CAGTGCCGAG	AGTTTCAGTA	CA ATG	595
Met						
TGG AAA	TGG ATA	CTG ACA	CAT TGT	GCC TCA	TTC CCC	643
Trp Lys	Trp Trp	Ile Leu	Thr His	Cys Ala	Ser Ala	
				Phe	Pro	His
				Leu	Pro	
GGC TGC	TGC TGC	TGC TGC	TTT TTG	TTG CTG	TTC TTG	691
Gly Cys	Cys Cys	Cys Cys	Phe Leu	Leu Leu	Phe Leu	
				Val	Ser	Ser
				Val	Ser	Val
CCT GTC	ACC TGC	CAA GCC	CTT GGT	CAG GAC	ATG ATG	739
Pro Val	Thr Cys	Gln Ala	Leu Gly	Gln Asp	Met Val	
				Ser	Ser	Pro
				Pro	Glu	Ala
ACC AAC	TCT TCC	TCC TCC	TTC TCC	TCT CCT	TCC AGC	787
Thr Asn	Ser Ser	Ser Ser	Ser Phe	Ser Ser	Pro Ser	
				Asn	Ser	Gly
				Ala	Gly	Arg
CAT GTG	CGG AGC	TAC AAT	CAC CTT	CAA GGA	GAT GTC	835
His Val	Arg Ser	Tyr Asn	His Leu	Gln Gly	Asp Val	
				Asp	Arg	Trp
				Val	Arg	Arg
				Trp	Arg	Lys
CTA TTC	TCT TTC	ACC AAG	TAC TTT	CTC AAG	ATT GAG	883
Leu Phe	Ser Phe	Thr Tyr	Leu Lys	Ile Glu	Lys Asn	
				Ile	Gly	Lys
				Gl	Asn	Gly
				Ile	Gly	Lys
GTC AGC	GGG ACC	AAG AAG	GAG AAC	TGC CCG	TAC AGC	931
Val Ser	Gly Thr	Lys Lys	Glu Asn	Cys Pro	Tyr Ser	
				Ile	Ile	Ile
				Leu	Leu	Leu
				Gl	Gl	Gl
ACA TCA	GTA GAA	ATC GGA	GTT GTT	GCC GTC	AAA GCC	979
Thr Ser	Val Glu	Ile Gly	Val Val	Ala Val	Val Ala	
				Ile	Ile	Asn
				Asn	Ser	Asn
TAT TAC	TTA GCC	ATG AAC	AAG AAG	GGG AAA	CTC TAT	1027
Tyr Tyr	Leu Ala	Met Asn	Lys Lys	Gly Lys	Leu Tyr	
				Leu	Gly	Ser
				Tyr	Ser	Lys
				Gl	Gl	Gl
TTT AAC	AAT GAC	TGT AAG	CTG AAG	GAG AGG	ATA GAG	1075
Phe Asn	Asn Asp	Cys Lys	Leu Lys	Glu Arg	Ile Glu	
				Ile	Gl	Asn
				Gl	Gl	Gly
				Tyr	Tyr	Tyr

FIG.3A

AAT ACC TAT GCA TCA TTT AAC TGG CAG CAT AAT GGG AGG CAA ATG TAT	1123
Asn Thr Tyr Ala Ser Phe Asn Trp Glu His Asn Glu Arg Glu Met Tyr	
GTG GCA TTG AAT GGA AAA GGA GCT CCA AGG AGA GGA CAG AAA ACA CGA	1171
Val Ala Leu Asn Glu Lys Glu Ala Pro Arg Arg Glu Glu Lys Thr Arg	
AGG AAA AAC ACC TCT GCT CAC TTT CTT CCA ATG GTG GTA CAC TCA	1216
Arg Lys Asn Thr Ser Ala His Phe Leu Pro Met Val Val His Ser	
TAGAGGAAGG CAACGTTGT GGATGCAGTA AAACCAATGG CTCTTTGCC AAGAATAGTG	1276
GATATTCTTC ATGAAGACAG TAGATTGAAA GGCAAAGACA CGTTGCAGAT GTCTGCTTGC	1336
TTAAAAGAAA GCCAGCCTT GAAGGTTTT GTATTCACTG CTGACATATG ATGTTCTTT	1396
AATTAGTTCT GTGTCAATGTC TTATAATCAA GATATAGGCA GATCGAATGG GATAGAAGTT	1456
ATTCCCAAGT GAAAAACATT GTGGCTGGGT TTTTGTTGT TGTTGTCAAG TTTTGTTTT	1516
TAAACCTCTG AGATAGAACT TAAAGGACAT AGAACAAATCT GTTGAAAGAA CGATCTCGG	1576
GAAAGTTATT TATGGAATAC GAACTCATAT CAAAGACTTC ATTGCTCATT CAAGCCTAAT	1636
GAATCAATGA ACAGTAATAC GTGCAAGCAT TTACTGGAAA GCACTTGGGT CATATCATAT	1696
GCACAACCAA AGGAGTTCTG GATGTGGTCT CATGGAATAA TTGAATAGAA TTTAAAAATA	1756
TAAACATGTT AGTGTGAAAC TGTTCTAACAA ATACAAATAG TATGGTATGC TTGTGCATT	1816
TGCCTTCATC CCTTTCTATT TCTTCTAACAG TTATTTATT AATAGGATGT TAAATATCTT	1876
TTGGGGTTTT AAAGAGTATC TCAGCAGCTG TCTTCTGATT TATCTTTCT TTTTATTCAAG	1936
CACACCACAT GCATGTTCAC GACAAAGTGT TTTAAAAC TGGCGAACAC TTCAAAAATA	1996
GGAGTTGGGA TTAGGGAAGC AGTATGAGTG CCCGTGTGCT ATCAGTTGAC TTAATTGCA	2056
CTTCTGCAGT AATAACCATC AACAAATAAT ATGGCAATGC TGTGCCATGG CTTGAGTGAG	2116
AGATGTCTGC TATCATTGAA AACATATAT TACTCTCGAG GCTTCCTGTC TCAAGAAATA	2176
GACCAGAAGG CCAAATTCTT CTCTTCAAT ACATCAGTTT GCCTCCAAGA ATATACTAAA	2236
AAAAGGAAAAA TTAATTGCTA AATACATTAA AATAGCCTAG CCTCATTATT TACTCATGAT	2296
TTCTTGCCAA ATGTCATGGC GGTAAAGAGG CTGTCCACAT CTCTAAAAAC CCTCTGTAAA	2356
TTCCACATAA TGCATCTTTC CCAAAGGAAC TATAAAGAAT TTGGTATGAA GCGCAACTCT	2416

CCCAGGGGCT TAAACTGAGC AAATCAAATA TATACTGGTA TATGTGTAAC CATATACAAA	2476
AACCTGTTCT AGCTGTATGA TCTAGTCTTT ACAAAACCAA ATAAAACCTG TTTTCTGTAA	2536
ATTTAAAGAG CTTTACAAGG TTCCATAATG TAACCATATC AAAATTCAATT TTGTTAGAGC	2596
ACGTATAGAA AAGAGTACAT AAGAGTTTAC CAATCATCAT CACATTGTAT TCCACTAAAT	2656
AAATACATAA GCCTTATTG CAGTGTCTGT AGTGATTTA AAAATGTAGA AAAATACTAT	2716
TTGTTCTAAA TACTTTAAG CAATAACTAT AATAGTATAT TGATGCTGCA GTTTTATCTT	2776
CATATTCTT GTTTGAAAA AGCATTAT TGTTGGACA CAGTATTTG GTACAAAAAA	2836
AAAGACTCAC TAAATGTGTC TTACTAAAGT TTAACCTTG GAAATGCTGG CGTTCTGTGA	2896
TTCTCCAACA AACTTATTG TGTCAATACT TAACCAGCAC TTCCAGTTAA TCTGTTATT	2956
TTAAAAATTG CTTTATTAAG AAATTTTTG TATAATCCA TAAAAGGTCA TATTTTCCC	3016
ATTCTCAAA AAAACTGTAT TTCAGAAGAA ACACATTGA GGCACTGTCT TTTGGCTTAT	3076
AGTTAAATT GCATTTCATC ATACTTGCT TCCAACTTGC TTTTGGCAA ATGAGATTAT	3136
AAAAATGTTT AATTTTG GTTGGATCT GGATGTTAAA ATTTAATTGG TAACTCAGTC	3196
TGTGAGCTAT AATGTAATGC ATTCTATCC AAACCTAGGTA TCTTTTTTC CTTTATGTTG	3256
AAATAATAAT GGCACCTGAC ACATAGACAT AGACCACCA CAACCTAAAT TAAATGTTG	3316
GTAAGACAAA TACACATTGG ATGACCACAG TAACAGCAAA CAGGGCACAA ACTGGATTCT	3376
TATTCACAT AGACATTTAG ATTACTAAAG AGGGCTATGT GTAAACAGTC ATCATTATAG	3436
TACTCAAGAC ACTAAAACAG CTTCTAGCCA AATATATTAA AGCTTGCAGA GGCCAAAAAT	3496
AGAAAACATC TCCCCGTCT CTCCCACATT TCCCTCACAG AAAGACAAAA AACCTGCCTG	3556
GTGCAGTAGC TCACACCTGT AATCCCAGCA GTTGGGAGA CTGTGGGAAG ATGGCTTGAG	3616
TCCAGGAGTT CTAGACAGGC CTGAGAAACC TAGTGAGACA TCCTTCTCTT AAACAAAACA	3676
AAACAAAACA AATGTAGCCA TGCCTGGG CATATACCTG TGGTCCCAAC TACTCAGGAG	3736
GCTGAAACGG AAGGATCTCT TGGGCCAG GAGTTGAGG CTGCAGTGAG CTATAATCTT	3796
GCCATTGCAC TCCAGCCTGG GTGAAAAAGA GCCAGAAAGA AAGGAAAGAG AGAAAAGAGA	3856
AAAGAAAAGAG AGAAAAGACA GAAAGACAGG AAGGAAGGAA GGAAGGAAGG AAGGAAGGAA	3916
GGAAGCAAGG AAAGAAGGAA GGAAGGAAAG AAGGGAGGGA AGGAAGGAGA GAGAAAGAAA	3976
GATTGTTGG TAAGGAGTAA TGACATTCTC TTGCATTTAA AAGTGGCATA TTTGCTTGAA	4036

FIG.3C

ATGGAAATAG AATTCTGGTC CCTTTGCAA CTACTGAAGA AAAAAAAAAG CAGTTTCAGC	4096
CCTGAATGTT GTAGATTGA AAAAAAAA AAAAAAACTC GAGGGGGGGC CCGTACCCAA	4156
TTCGCCCTAT AGTGAGTCGT A	4177

**FIG.3D**

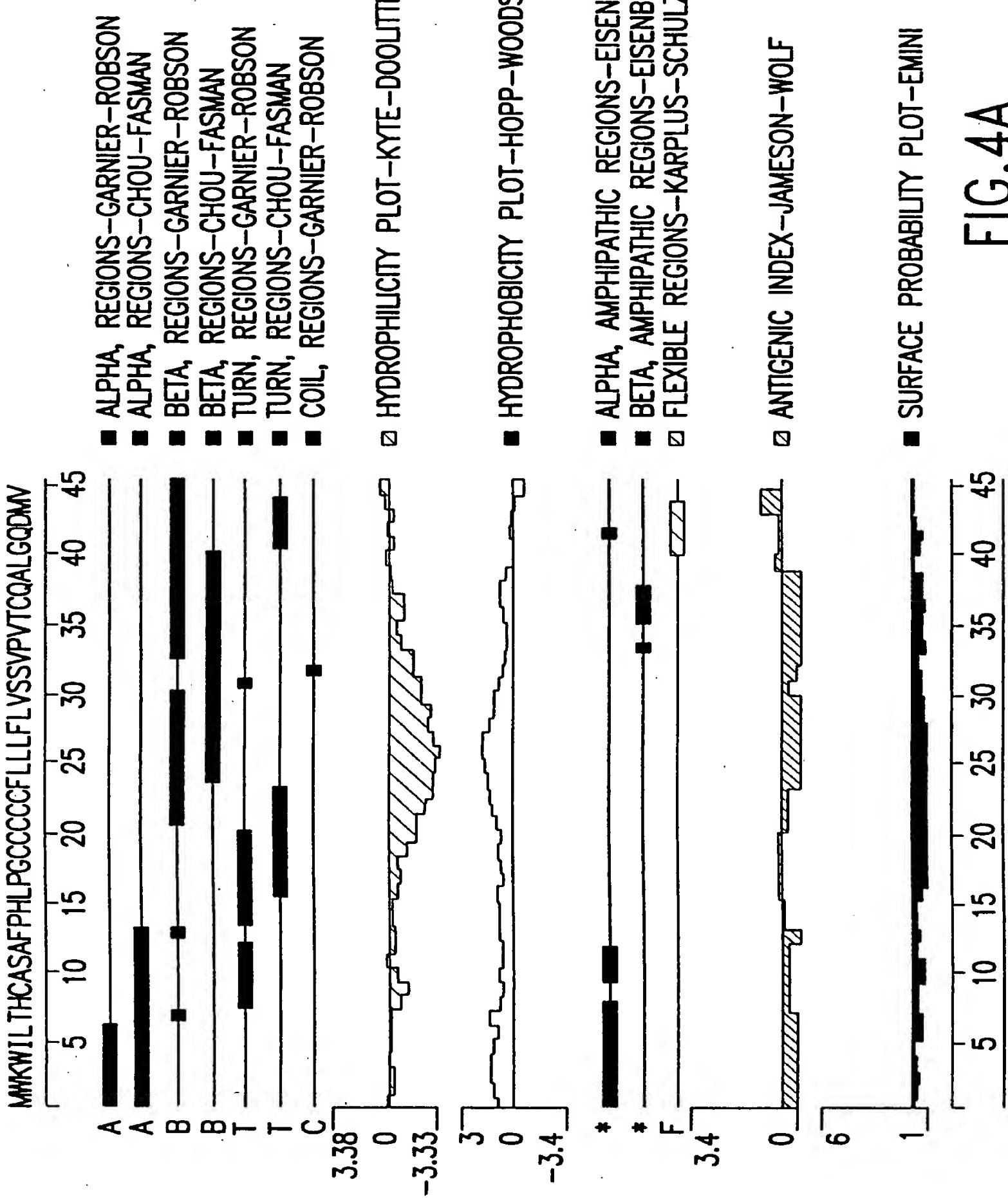
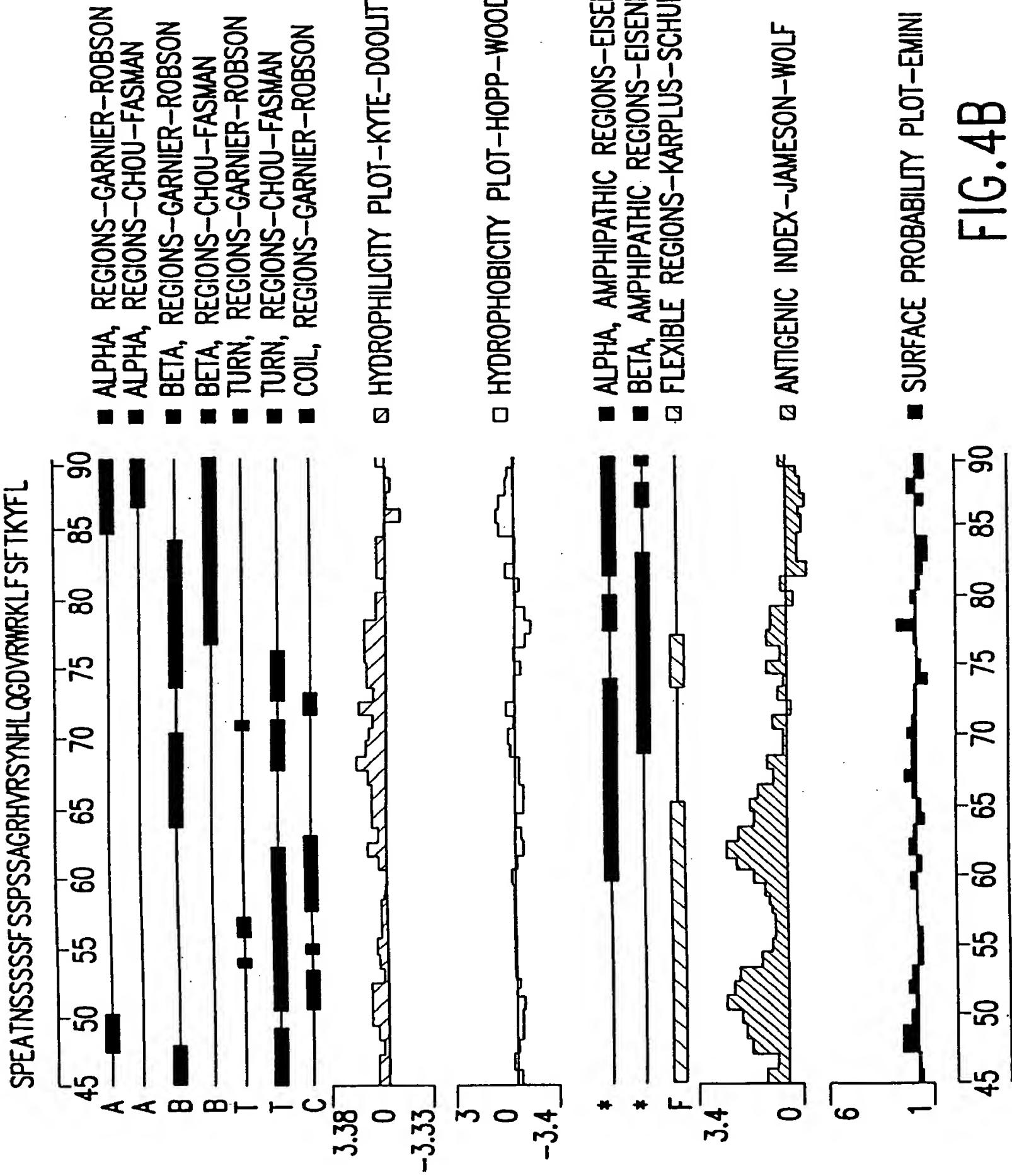


FIG. 4A



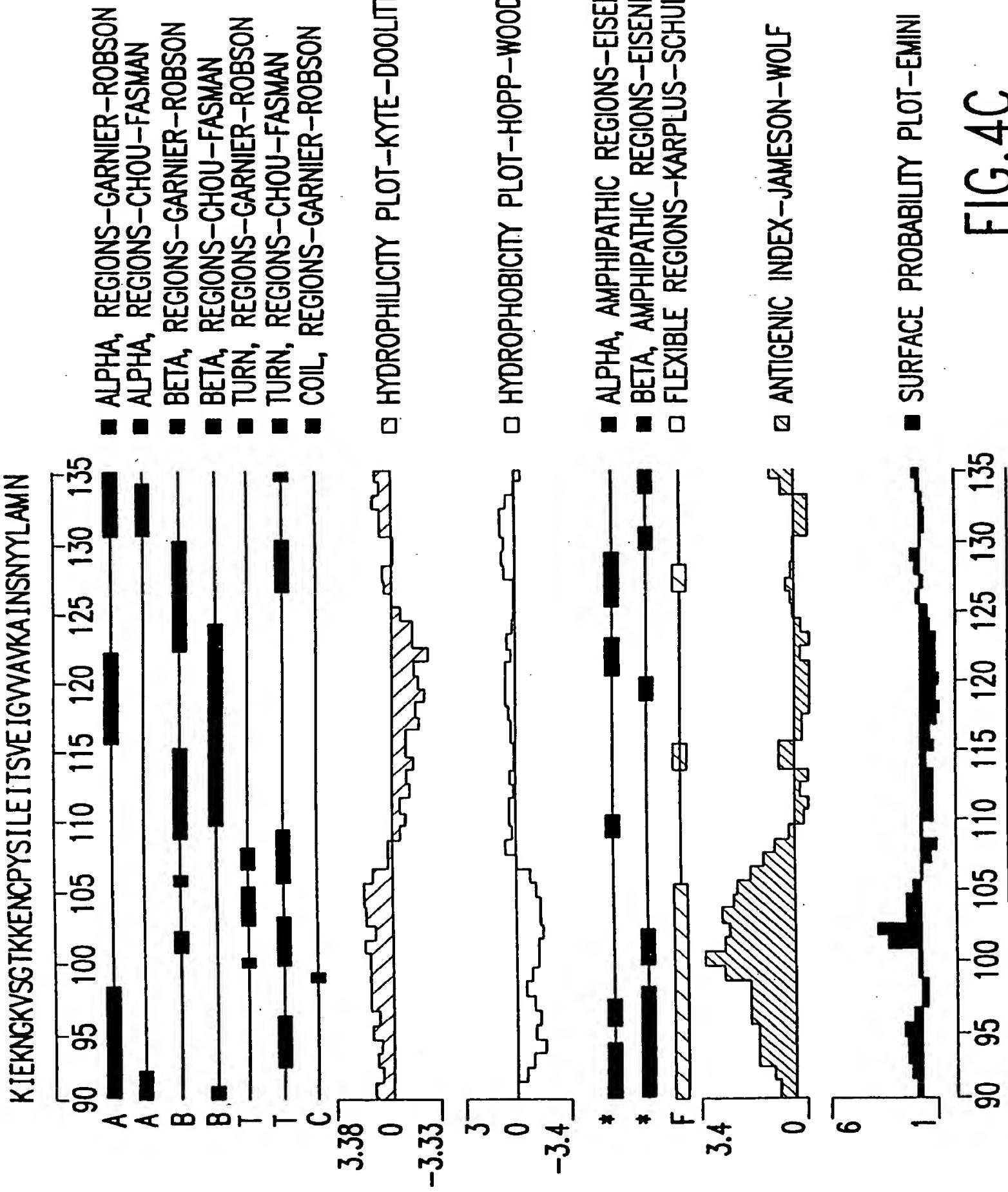
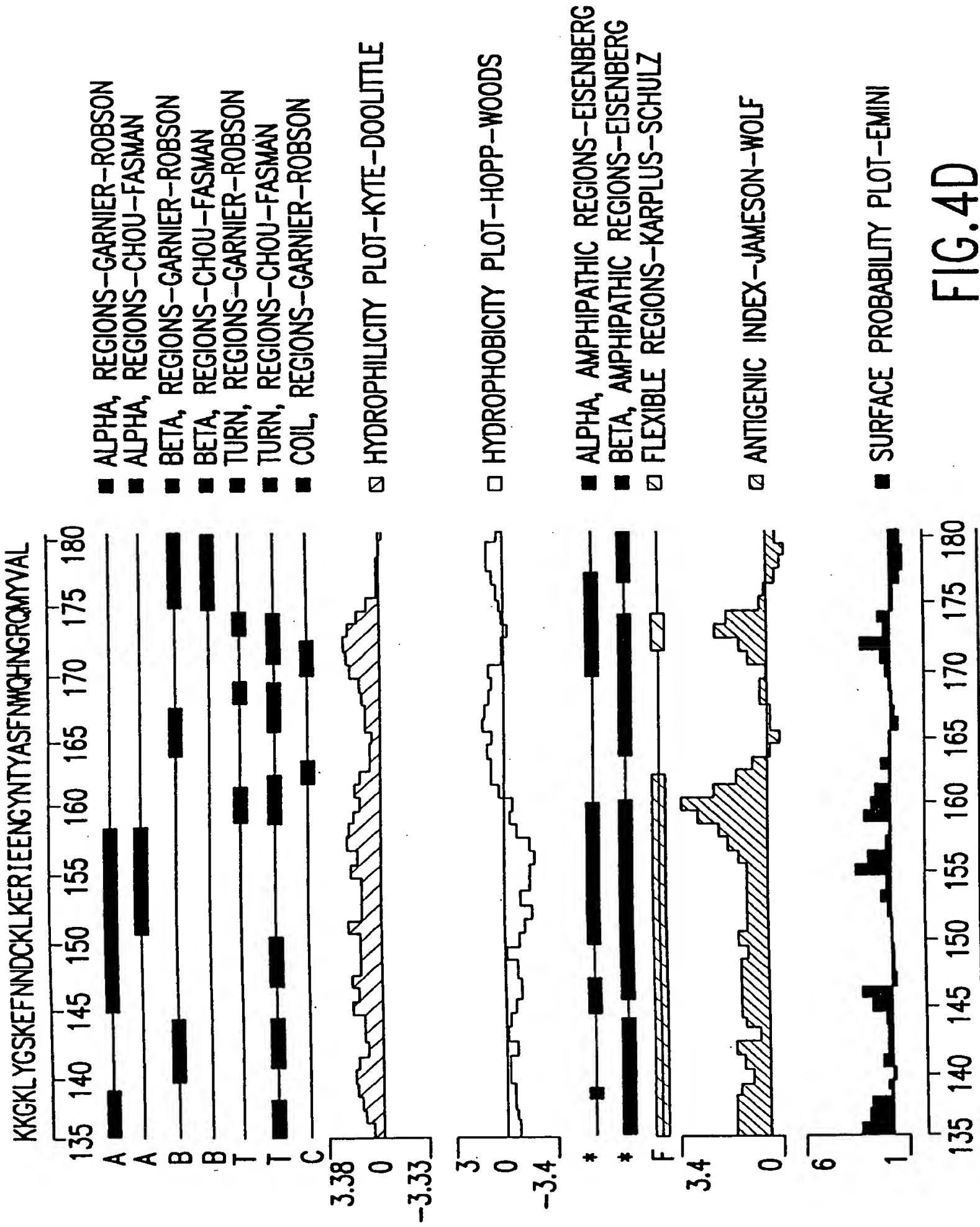


FIG. 4C



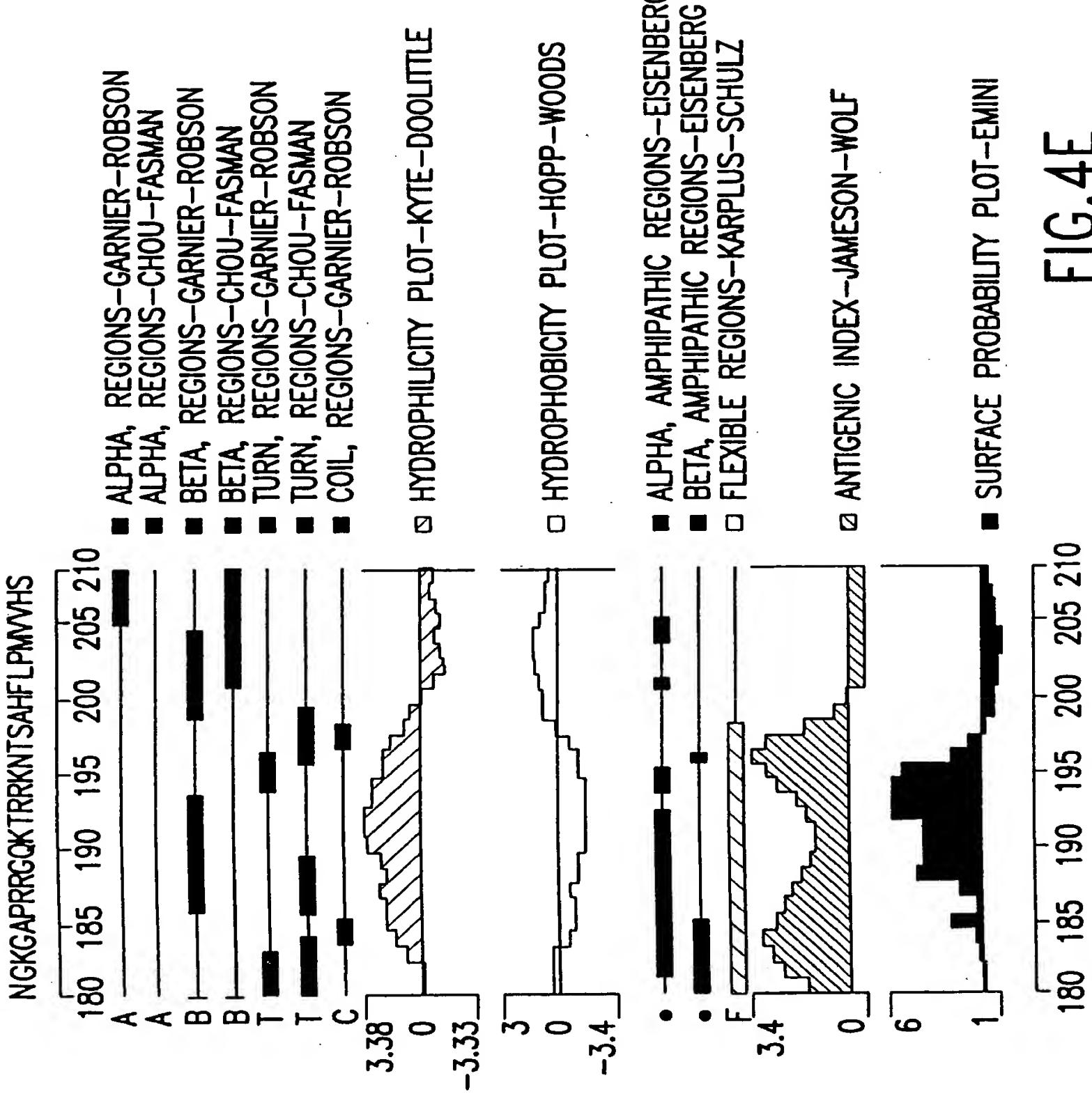


FIG. 4E

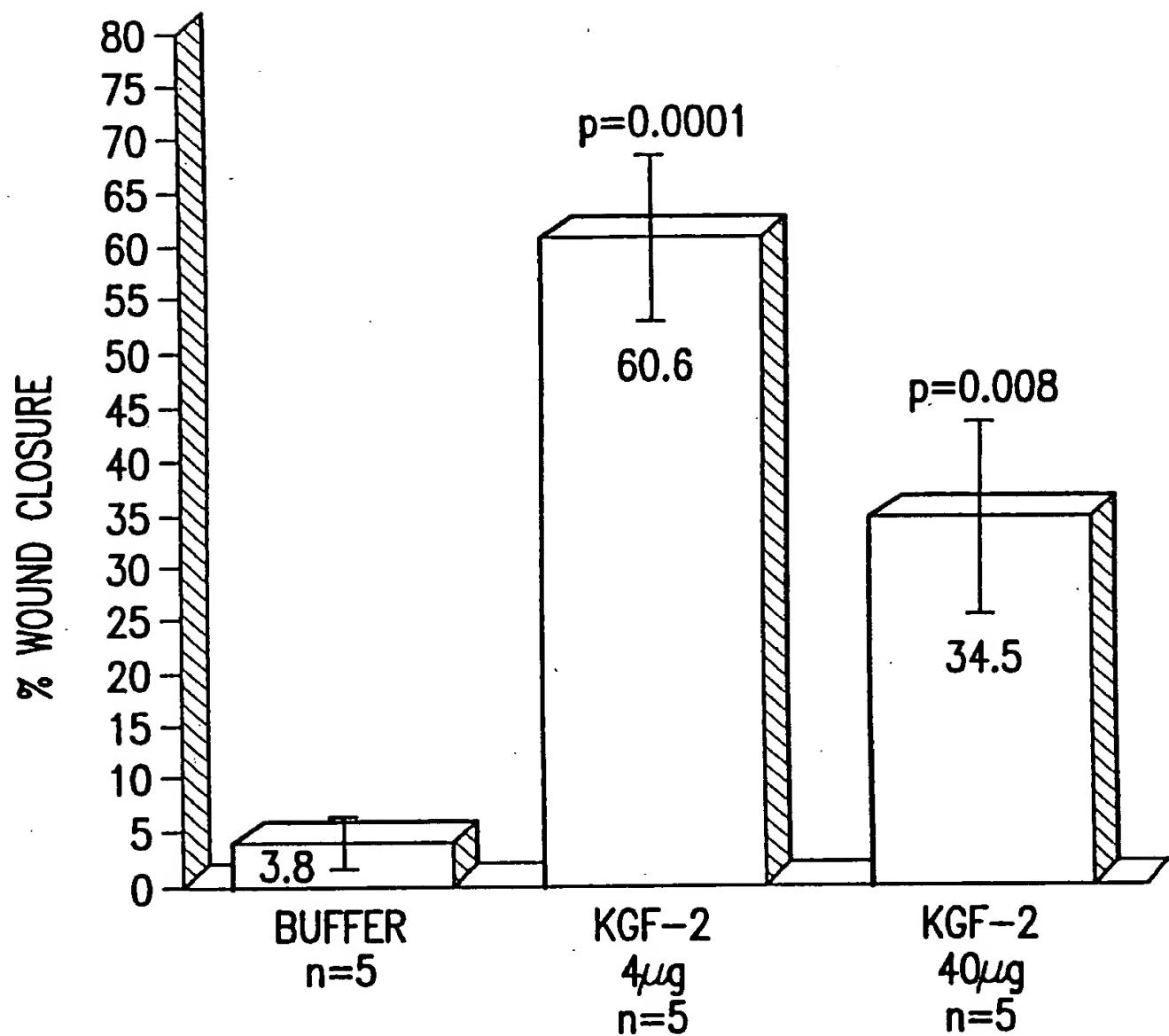


FIG.5

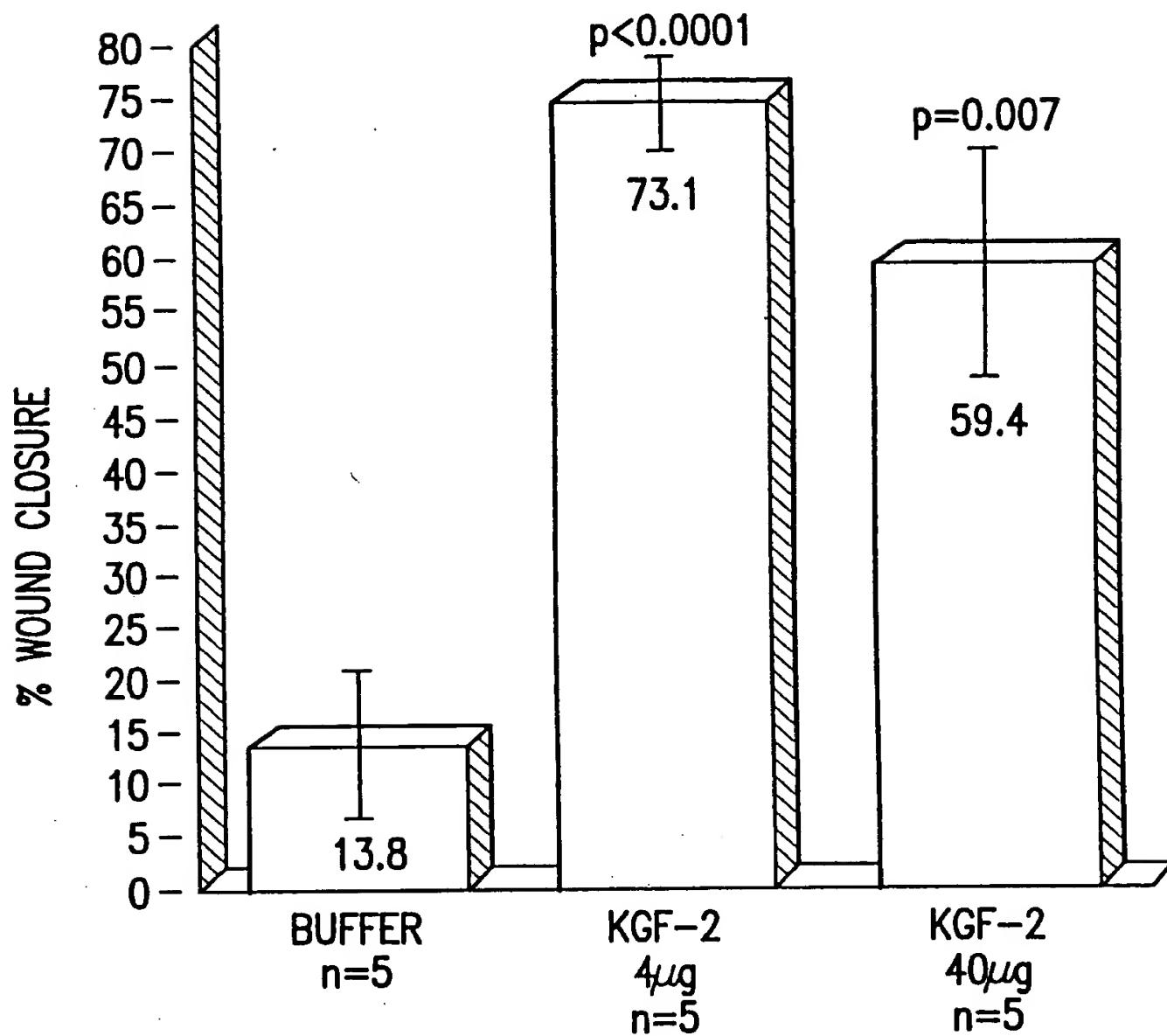


FIG. 6

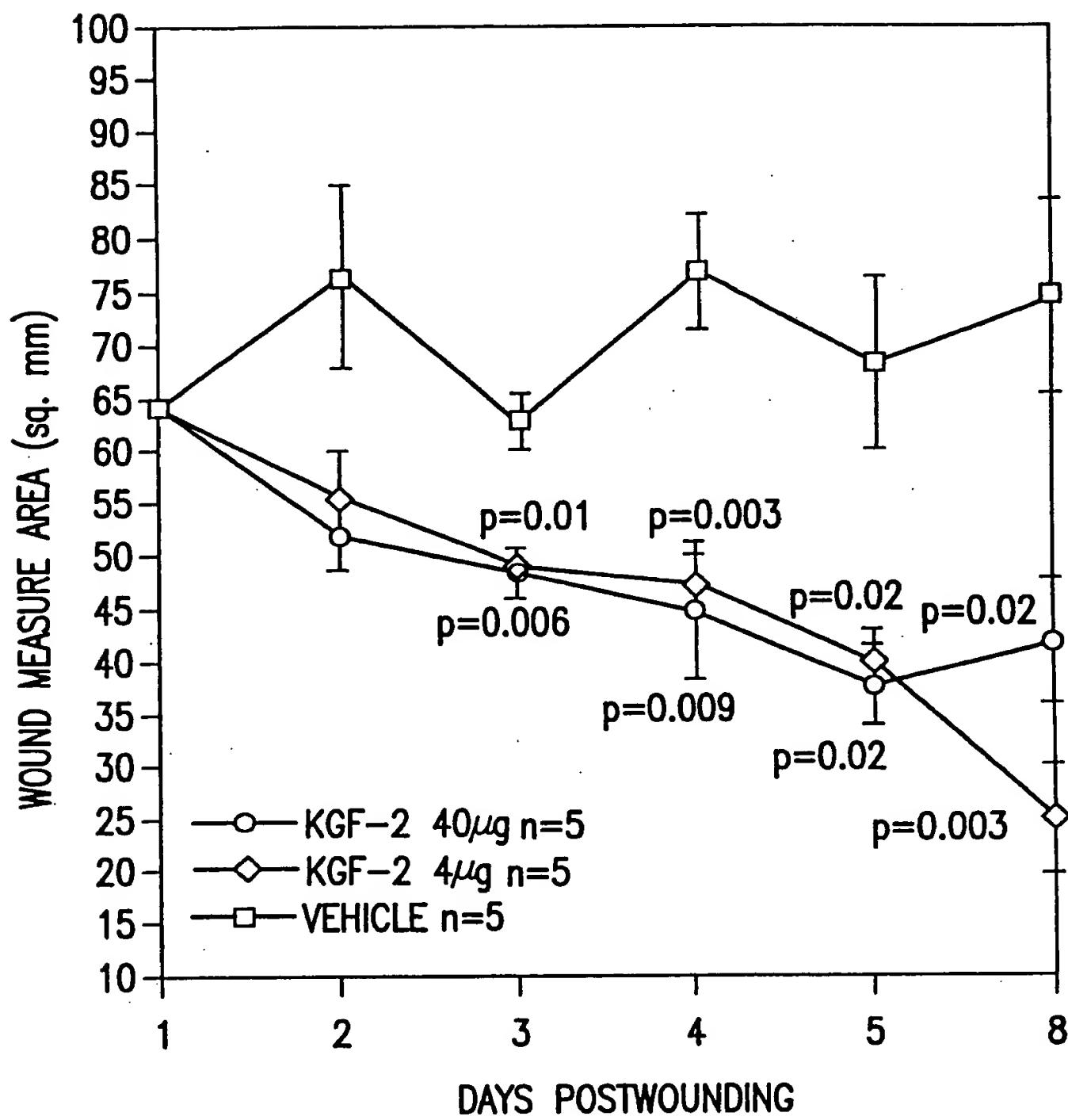
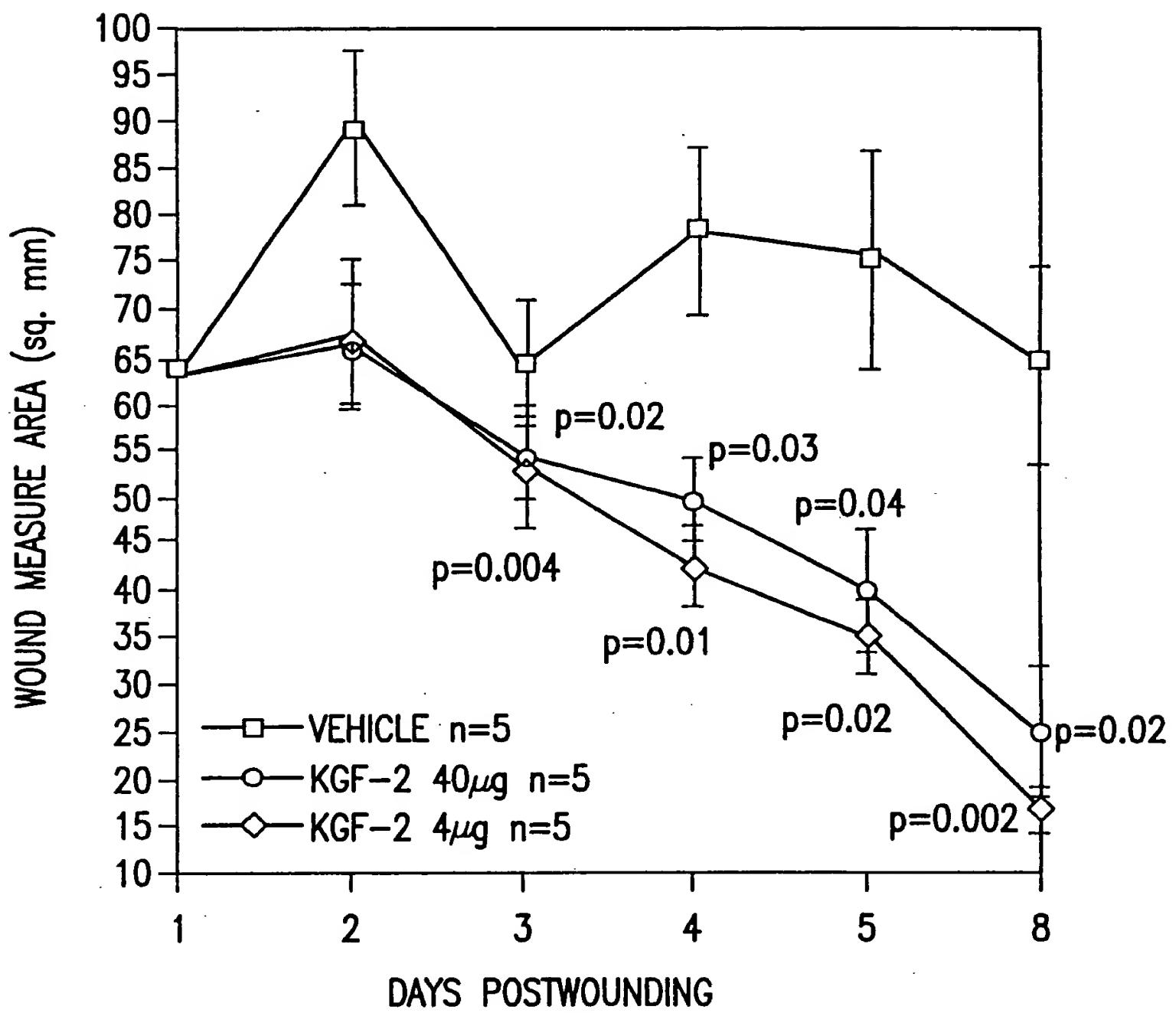
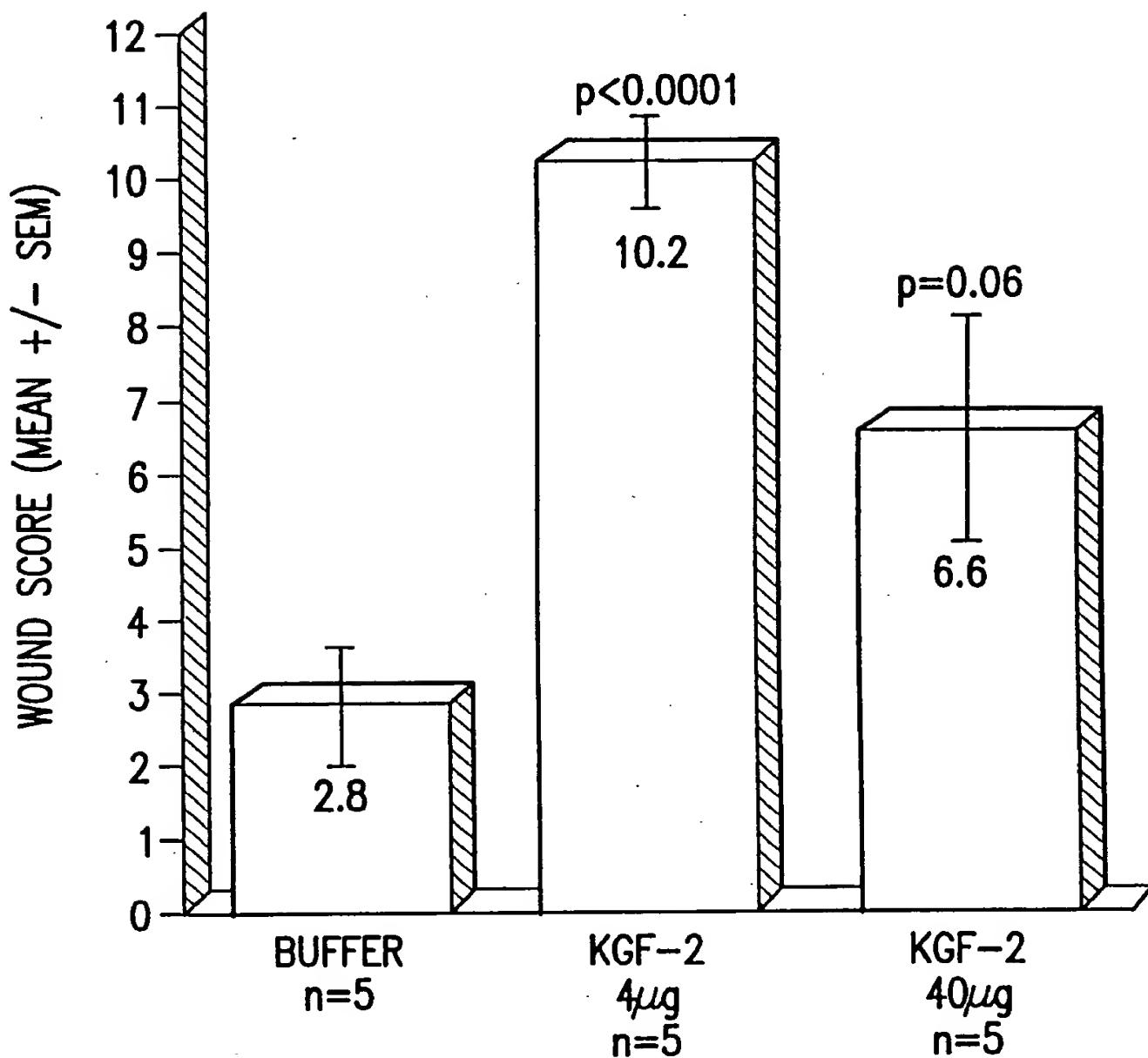


FIG.7

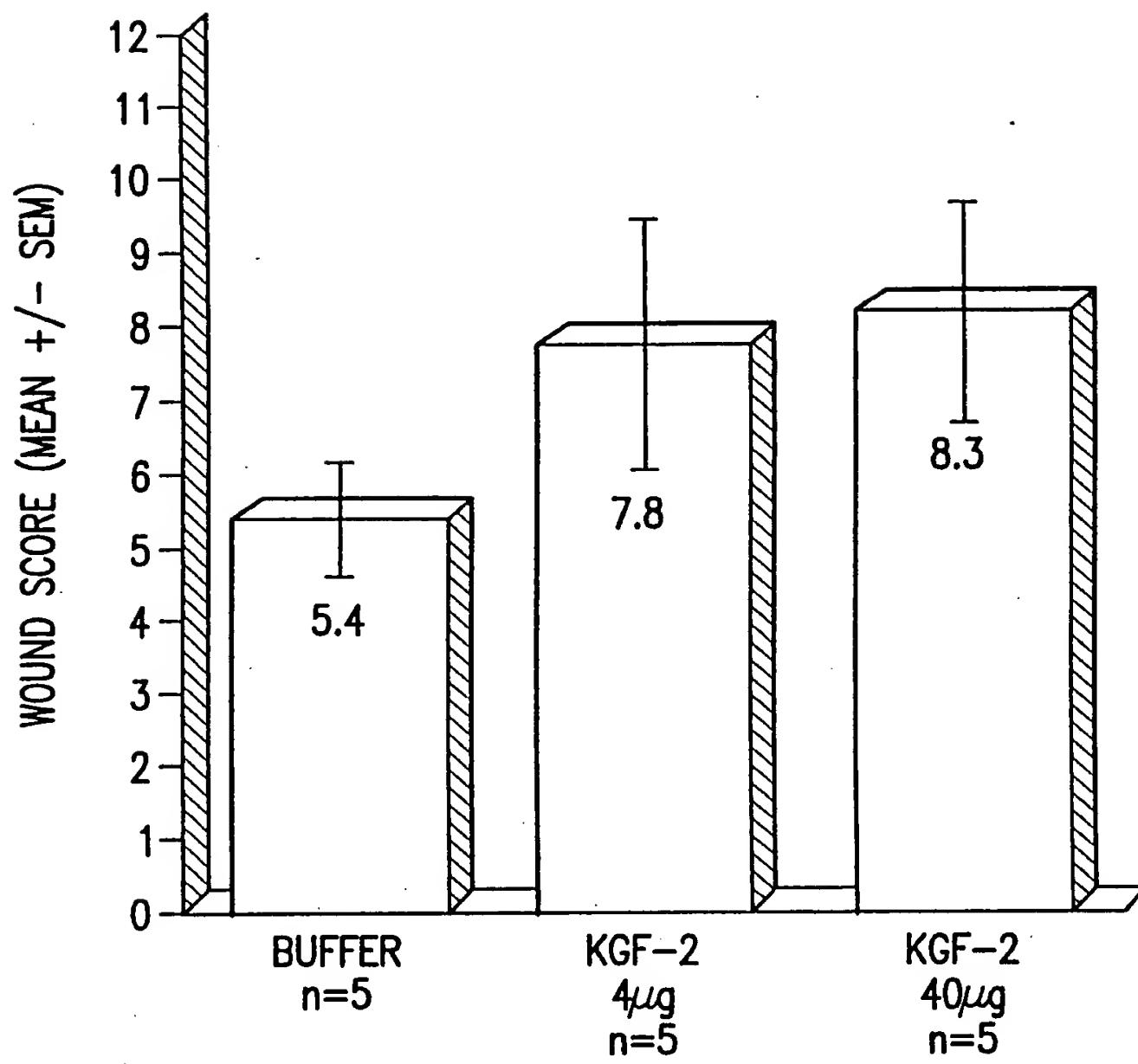


**FIG. 8**



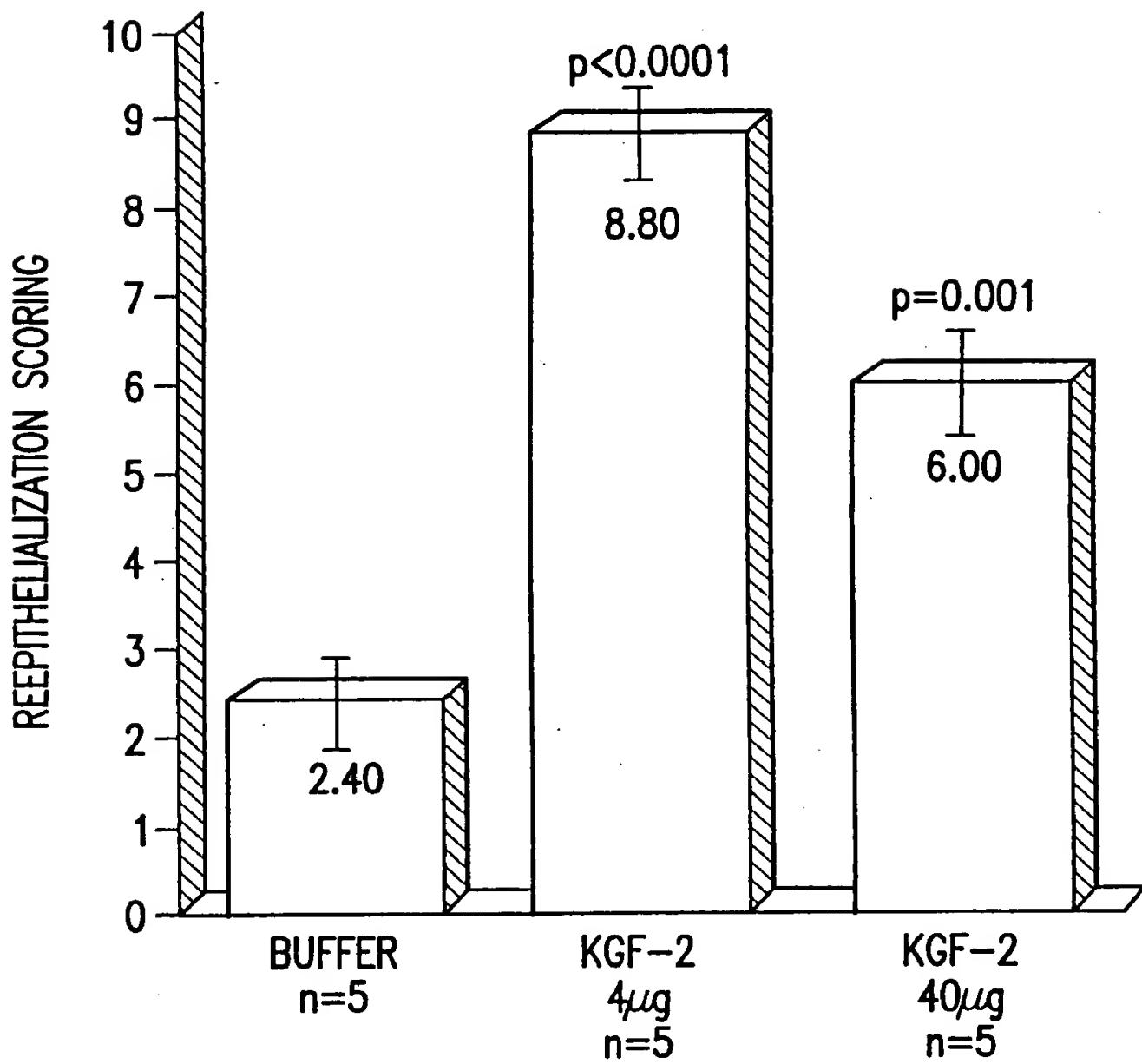
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.9



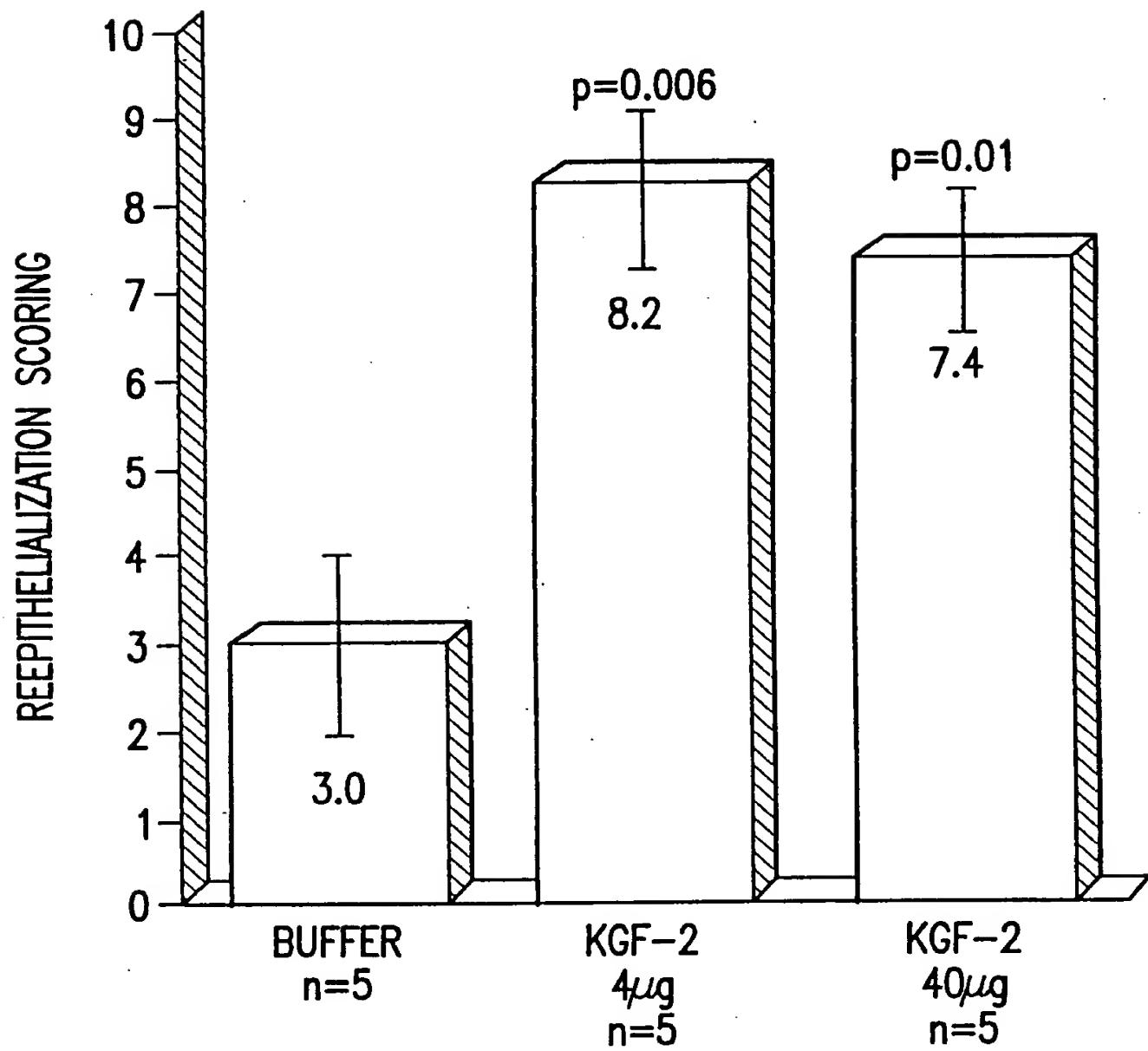
1-3 MINIMAL CELL ACCUMULATION, NO GRANULATION  
4-6 IMMATURE GRANULATION, INFLAMMATORY CELLS, CAPILLARIES  
7-9 GRANULATION TISSUE, CELLS, FIBROBLASTS, NEW EPITHELIUM  
10-12 FIBROBLASTS, COLLAGEN, EPITHELIUM

FIG.10



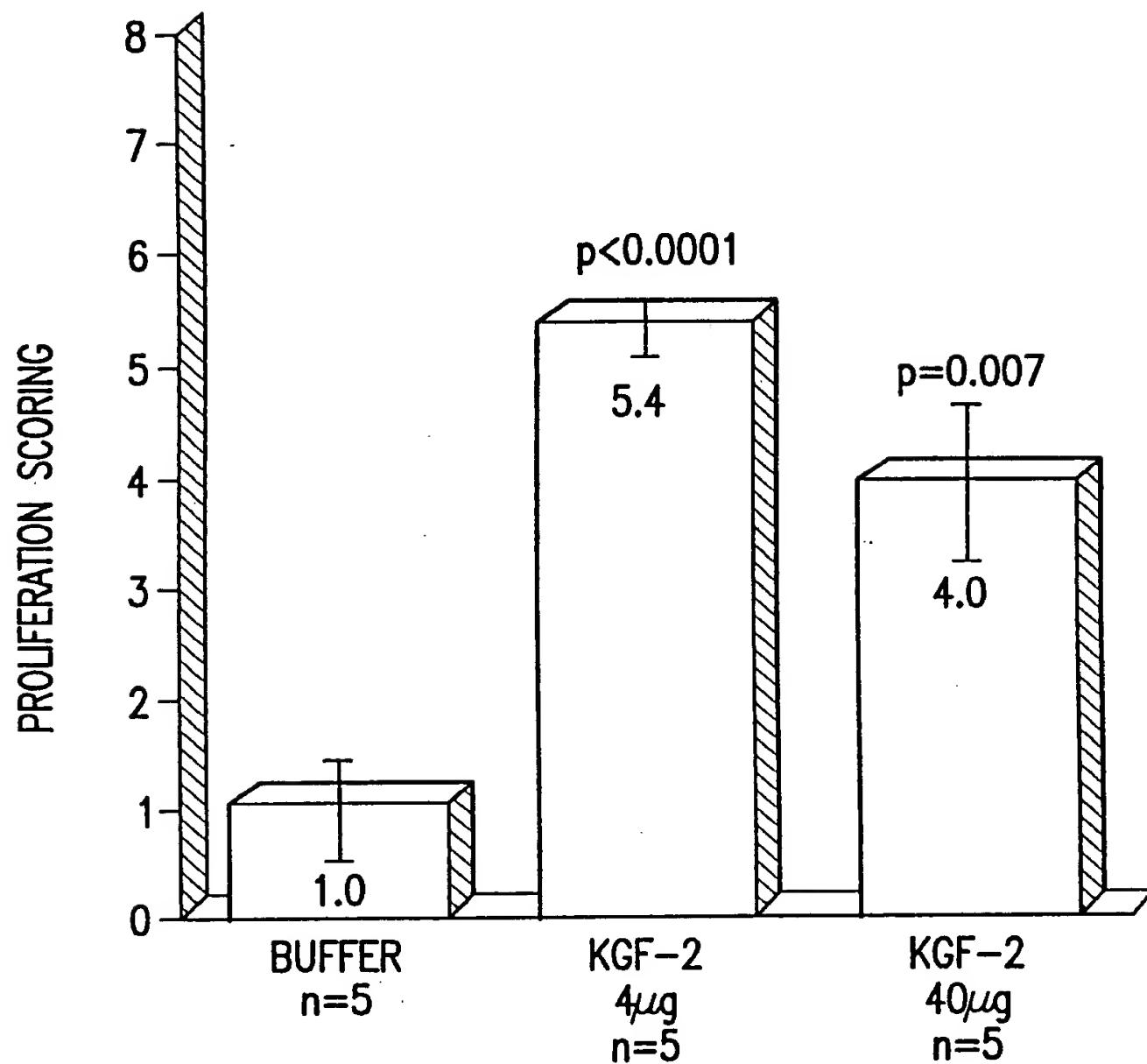
ANTI-CYTOKERATIN IMMUNOSTAINING  
0-NO CLOSURE  
5-SLIGHT TO MODERATE CLOSURE  
10-COMPLETE CLOSURE

FIG.11



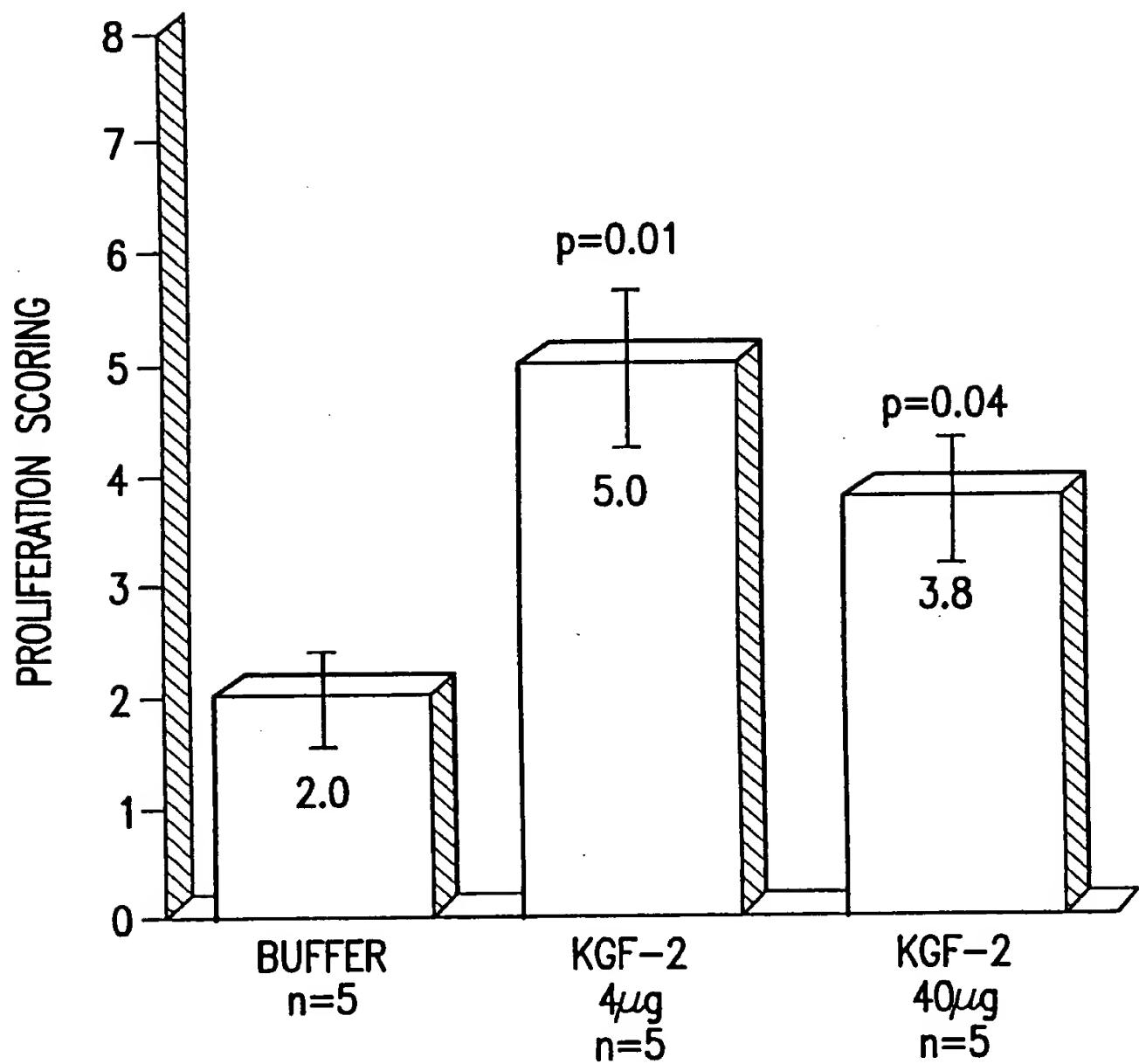
ANTI-CYTOKERATIN IMMUNOSTAINING  
0-NO CLOSURE  
5-SLIGHT TO MODERATE CLOSURE  
10-COMPLETE CLOSURE

FIG. 12



PCNA SCORING  
0-2 SLIGHT PROLIFERATION  
3-5 MODERATE PROLIFERATION  
6-8 INTENSE PROLIFERATION

FIG. 13



PCNA SCORING  
0-2 SLIGHT PROLIFERATION  
3-5 MODERATE PROLIFERATION  
6-8 INTENSE PROLIFERATION

FIG.14

ATGAGAGGATCGCATACCATCACCATCACGGATCCTGCCAGGCTCTGGGTC  
AGGACATGGTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTCTCTTCCC  
CGTCTTCCGCTGGTCGTACGTTCTTACAACCACCTGCAGGGTACGTTG  
GTTGGCGTAAACTGTTCTTTACCAAATACTTCCTGAAAATCGAAAAAA  
AACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCCGTACAGCATCCTG  
GAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAACAG  
CAACTATTACTAGCCATGAACAAGAAGGGAAACTCTATGGCTAAAAG  
AATTAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGAT  
ACAATACCTATGCATATTAACTGGCAGCATAATGGAGGCAAATGTAT  
GTGGCATTGAaTGGAAAAGGAGCTCCAaGGAGAGGACAGAAAACACGAAG  
GAAAAACACCTCTGCTCACTTCTCCAATGGTGGTACACTCATAG

MRGSHHHHHGSCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGD  
VRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSN  
YYLAMNKKGKLYGSKEFNNDKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVHS

kgf-2 synthetic cys37 Bam HI  
AAAGGATCCTGCCAGGCTCTGGTCAGGACATG

FIG.15

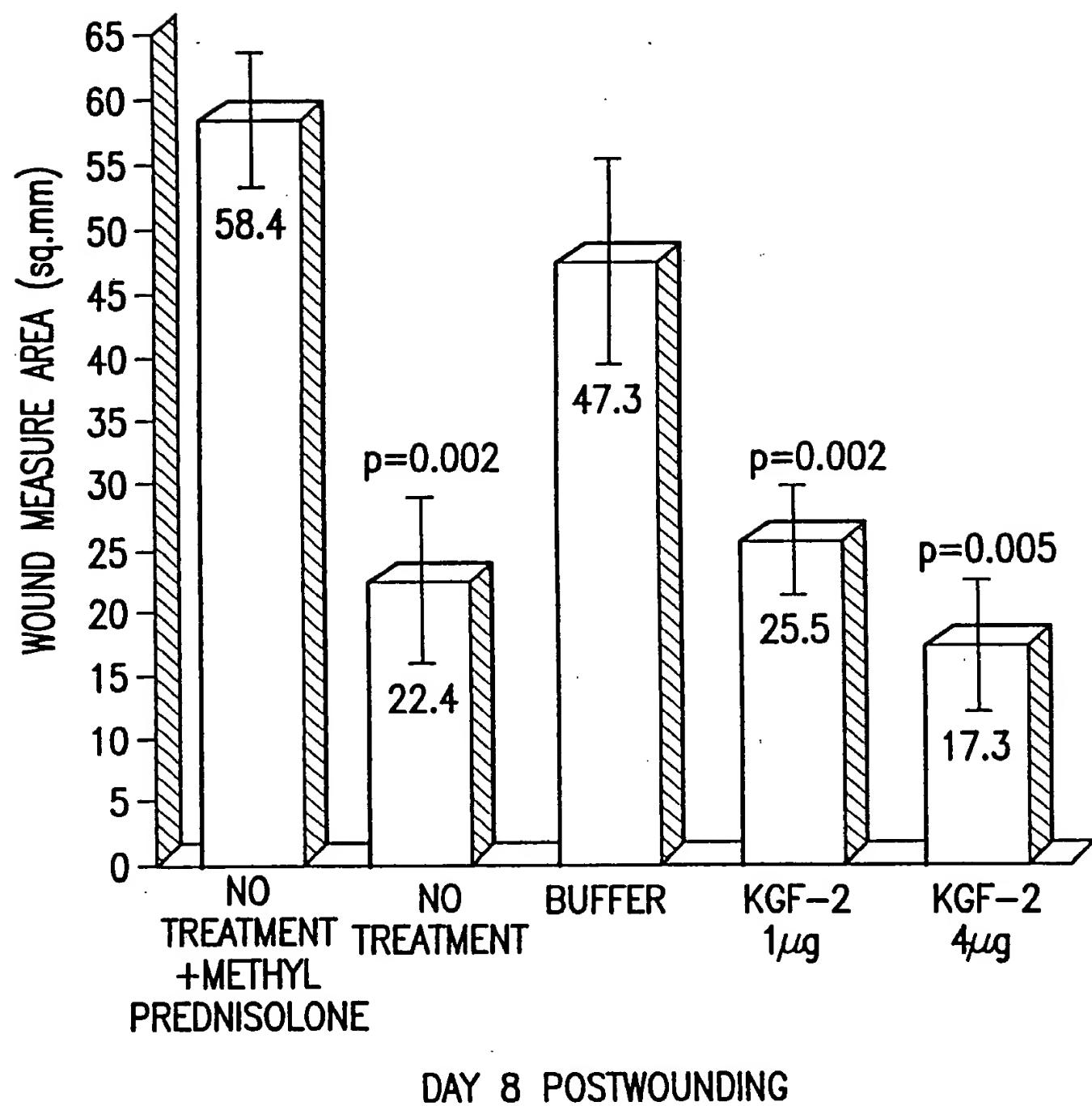
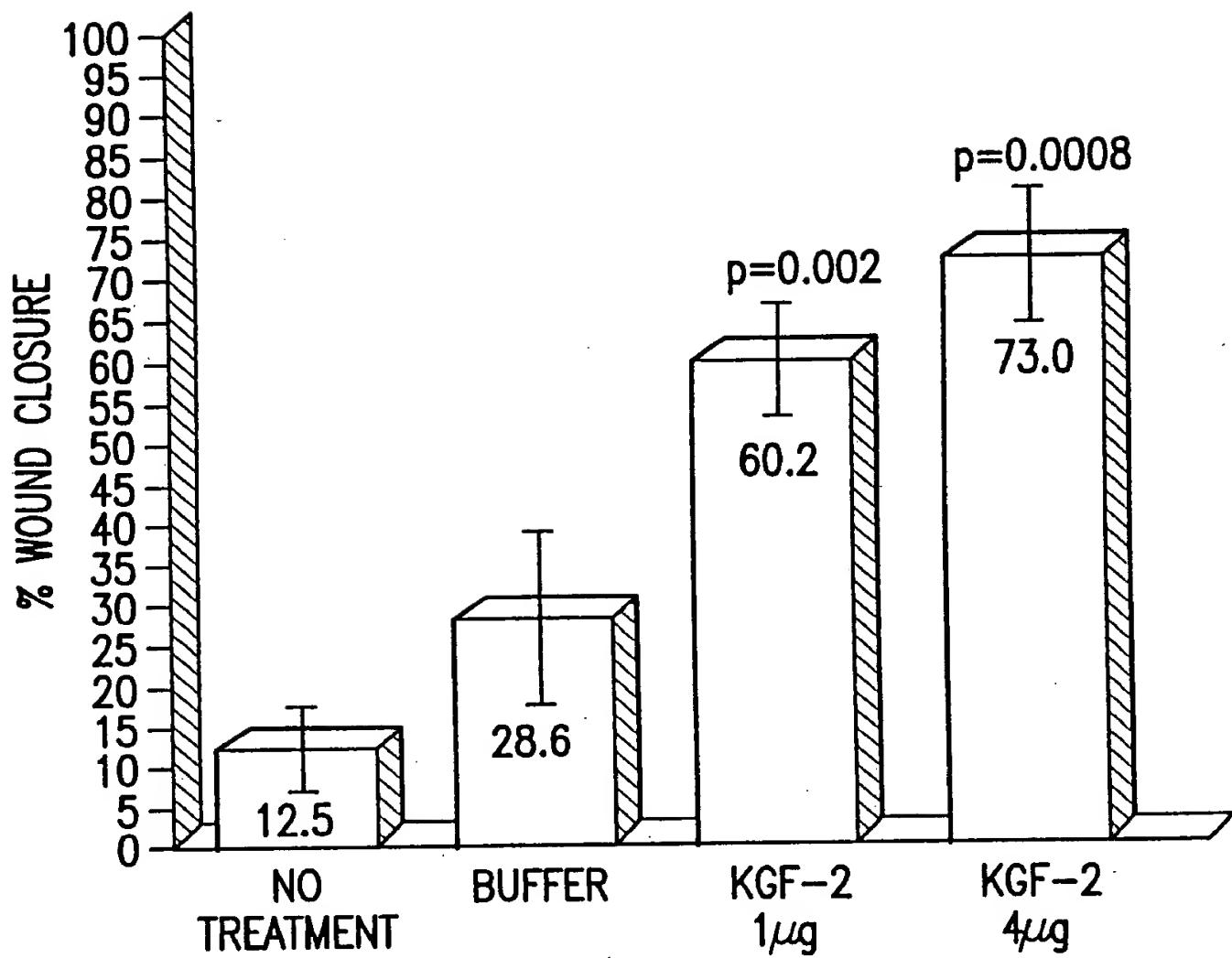


FIG. 16



GLUCOCORTICOID TREATED ANIMALS

FIG.17

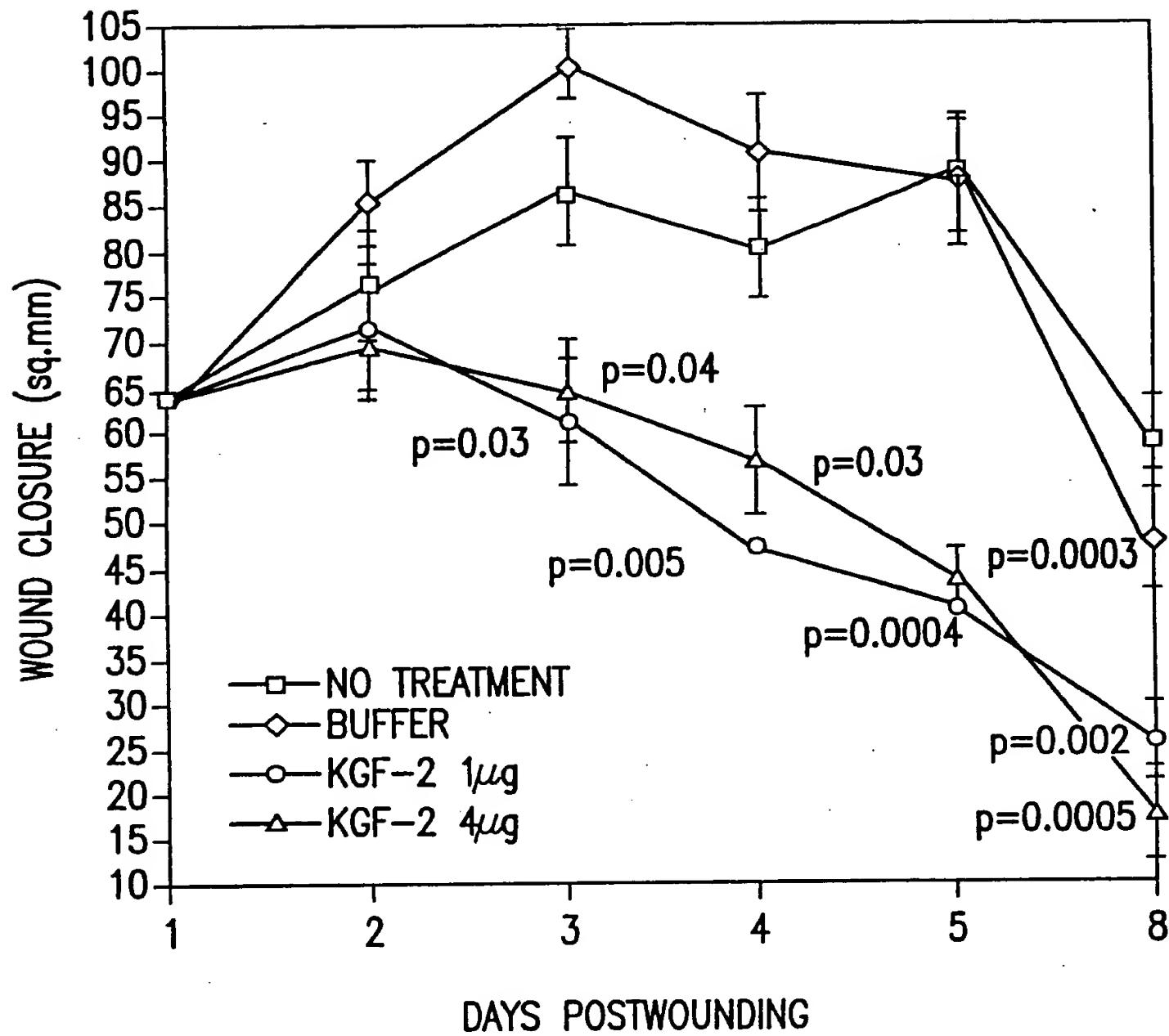


FIG. 18

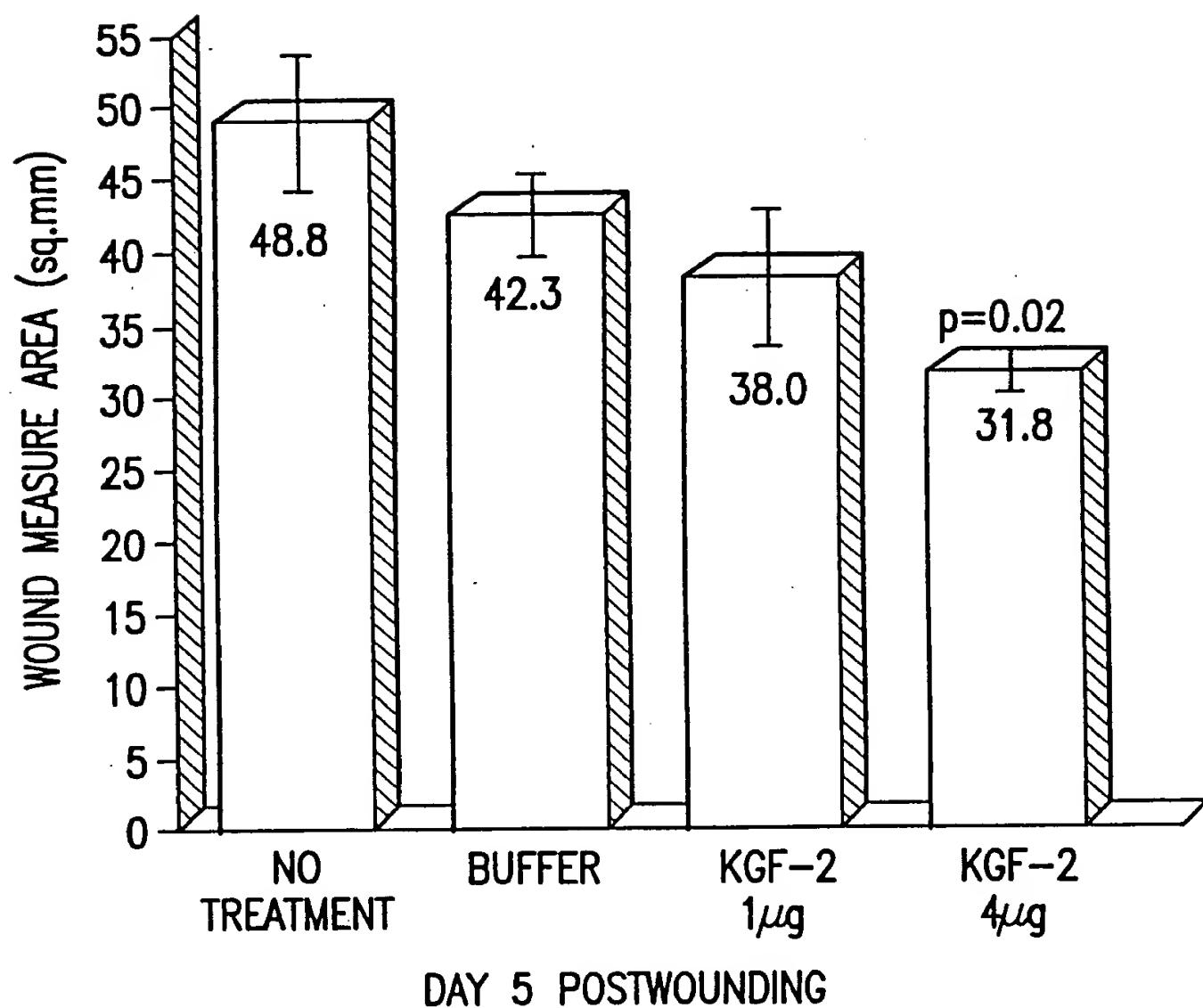
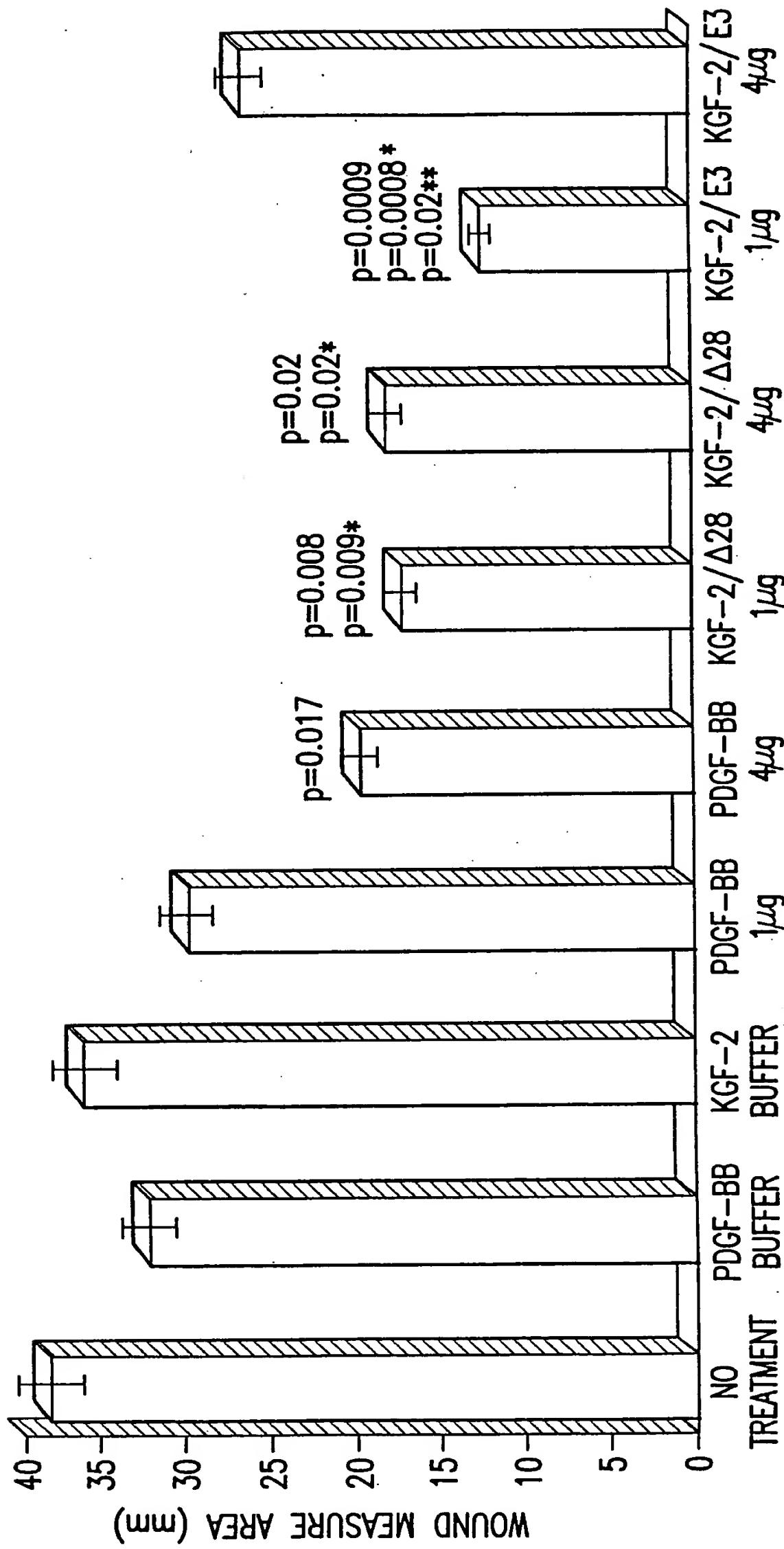
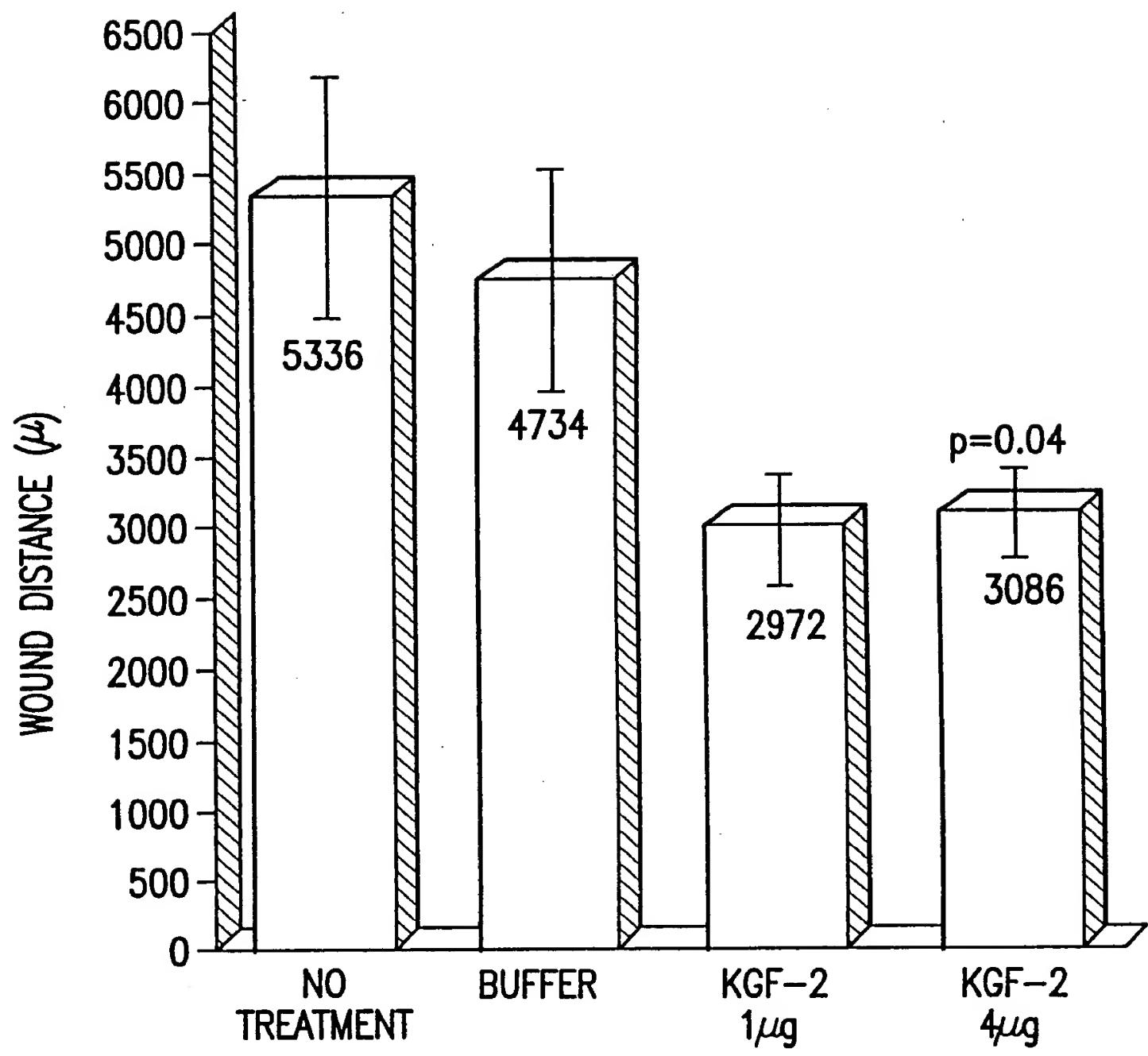


FIG. 19A



DAY 10 POSTWOUNDING

FIG. 19B



GLUCOCORTICOID TREATED GROUP

FIG.20

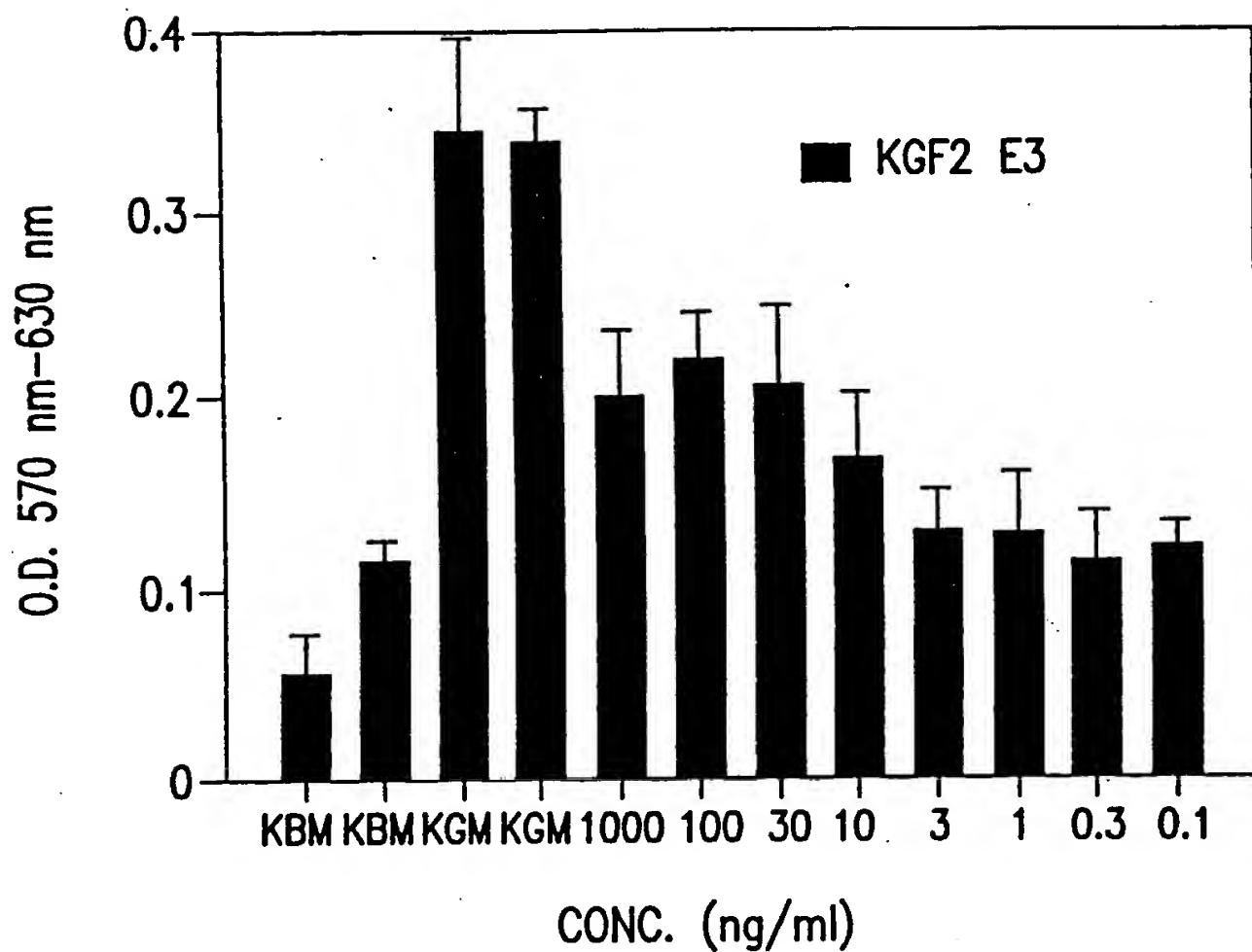


FIG.21A

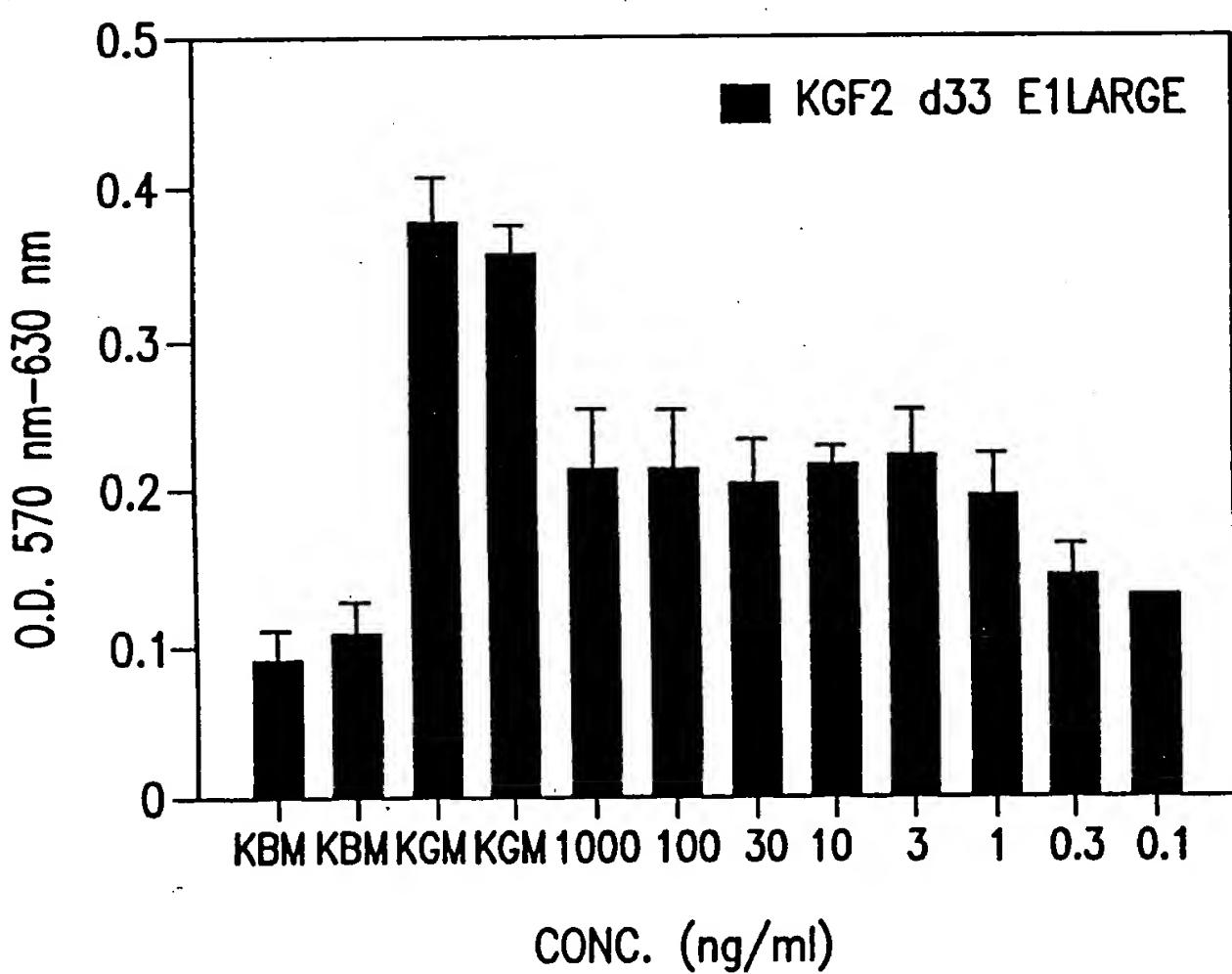


FIG.21B

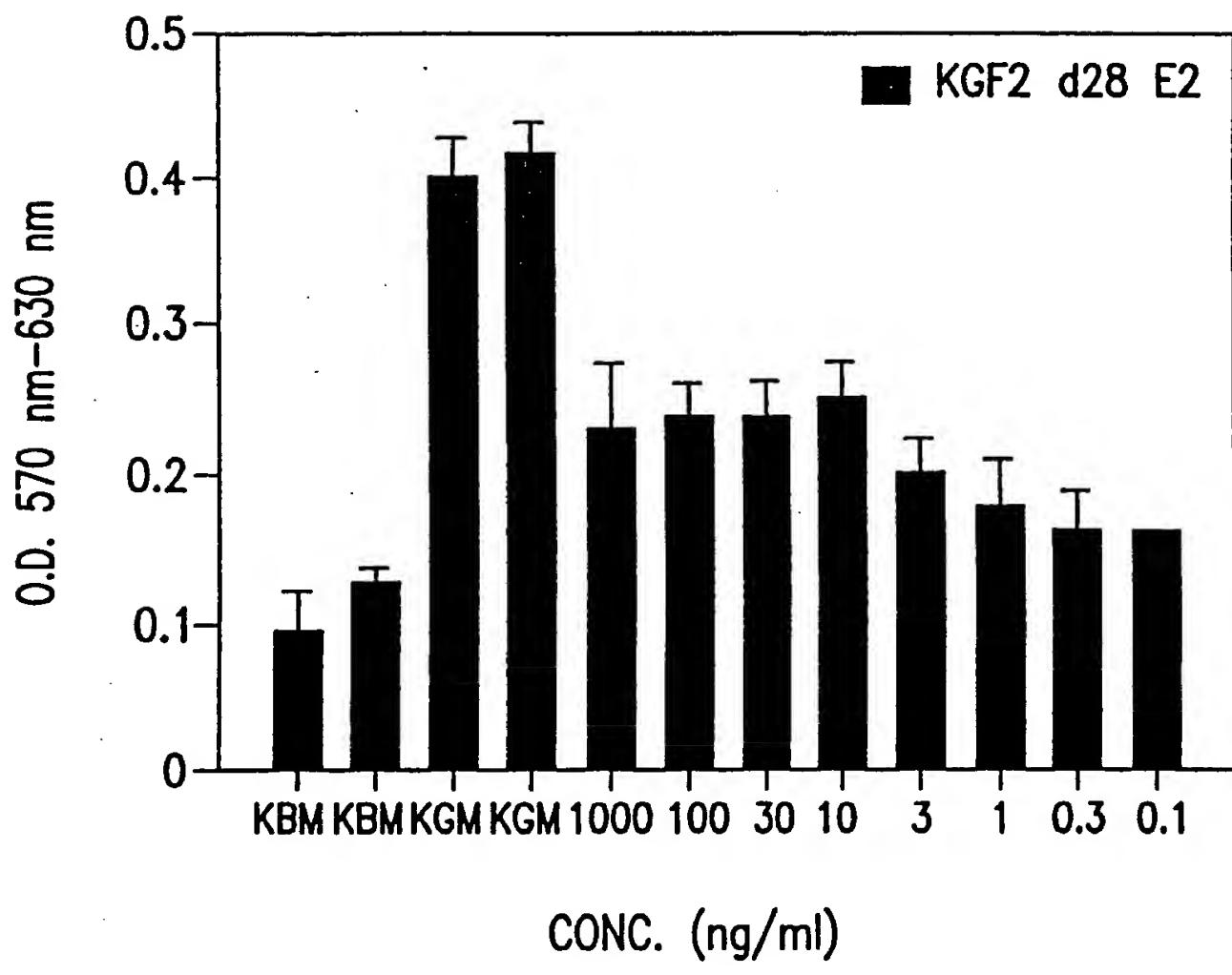


FIG.21C

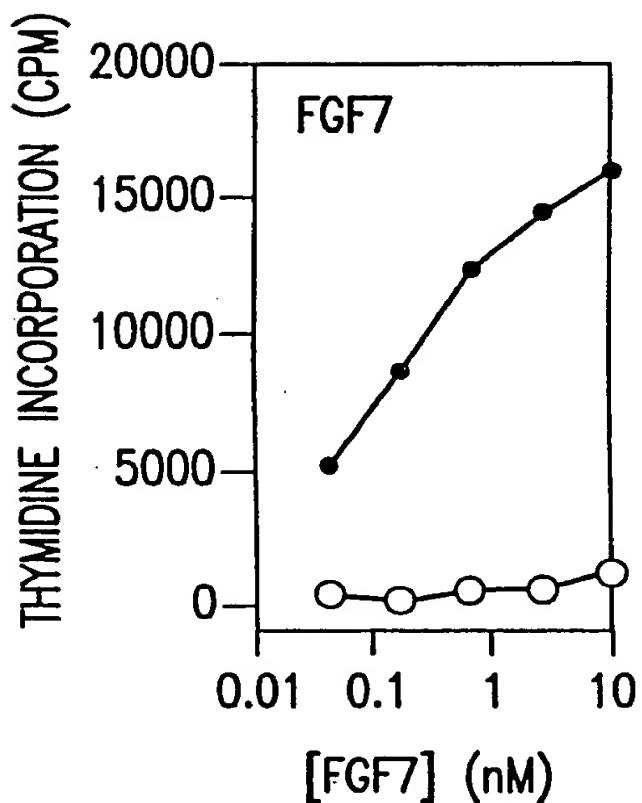


FIG.22A

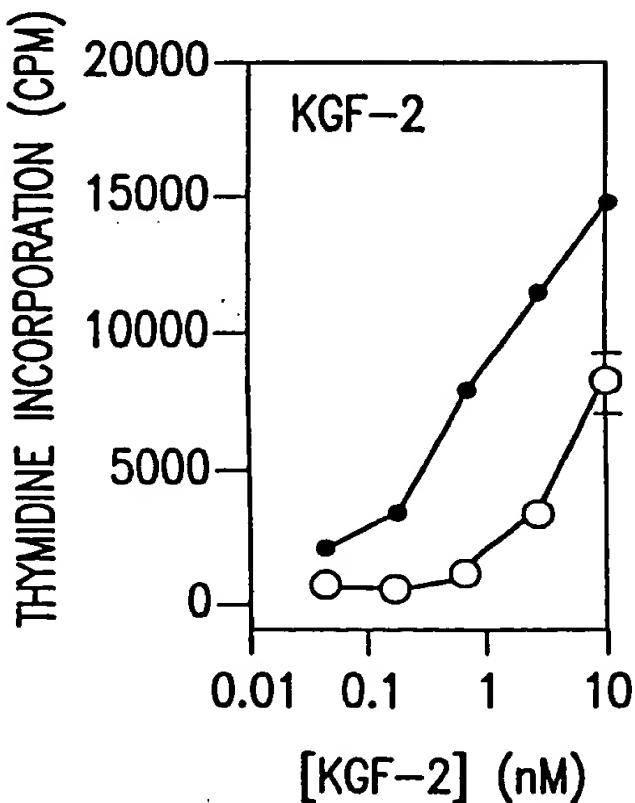


FIG.22A-1

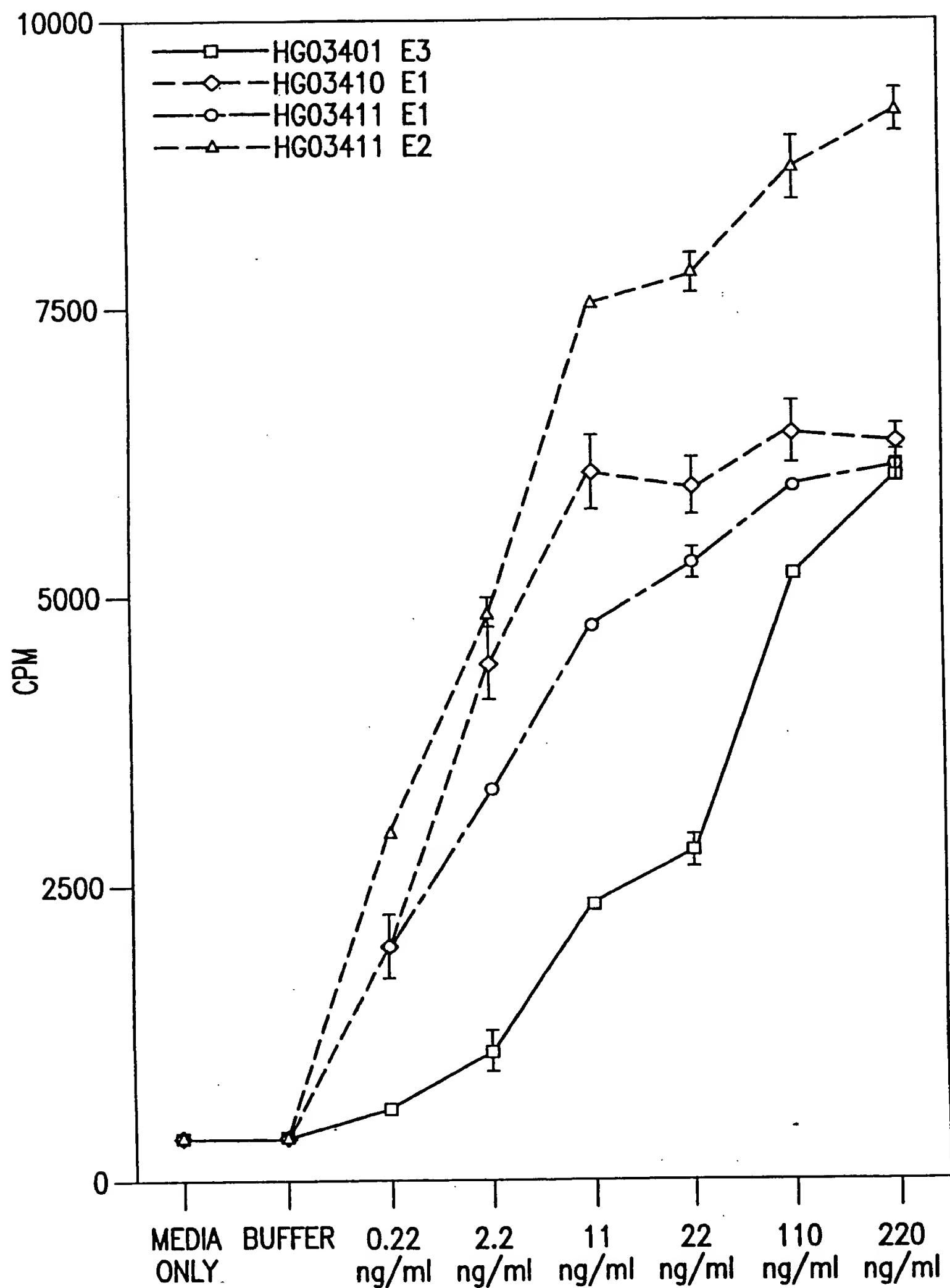


FIG.22B

BEST AVAILABLE COPY

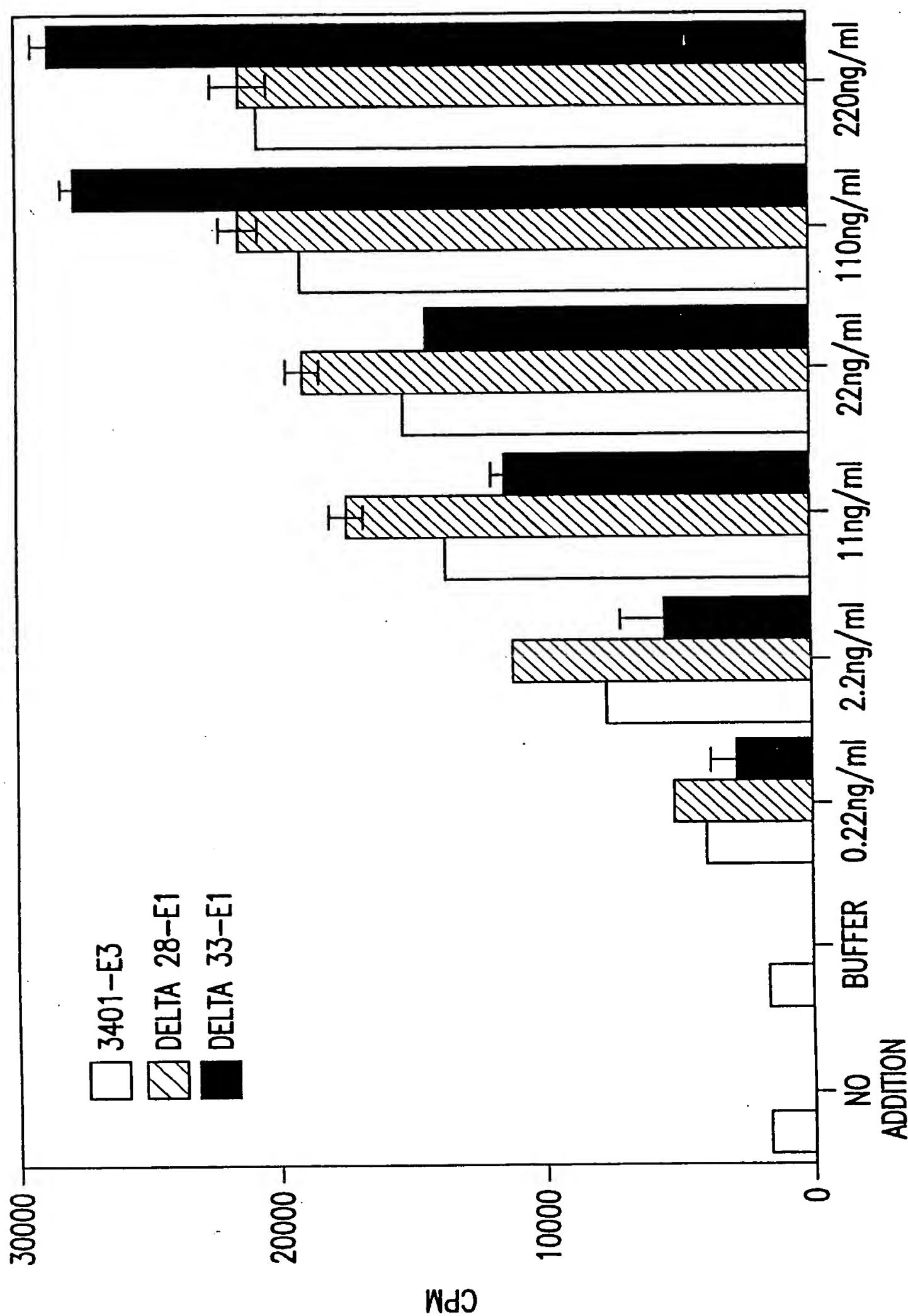


FIG. 22C

ATGTGGAAATGGATACTGACCCACTGCGCTCTGCTTCCGCACCTGCCGGGTTGCTG 60  
Met Trp Lys Trp Ile Leu Thr His Cys Ala Ser Ala Phe Pro His Leu Pro Gly Cys Cys  
|  
TGCTGCTGCTTCCTGCTGCTGTTCCCTGGTTCTTCTGTTCCGGTACCTGCCAGGCTCTG 120  
Cys Cys Cys Phe Leu Leu Phe Leu Val Ser Ser Val Pro Val Thr Cys Gln Ala Leu  
|  
GGTCAGGACATGGTTCTCCGGAAGCTACCAACTCTTCCTCTTCCTCTTCTTCCCCG 180  
Gly Gln Asp Met Val Ser Pro Glu Ala Thr Asn Ser Ser Ser Phe Ser Ser Pro  
|  
ACTTCCGCTGGTCGTACGTTCTTACAACCACCTGCAGGGTACGTTGGCGT 240  
Thr Ser Ala Gly Arg His Val Arg Ser Tyr Asn His Leu Gln Gly Asp Val Arg Trp Arg  
|  
AAACTGTTCTTTACCAAATACTTCCTGAAAATCGAAAAACGGTAAAGTTCTGGG 300  
Lys Leu Phe Ser Phe Thr Lys Tyr Phe Leu Lys Ile Glu Lys Asn Gly Lys Val Ser Gly  
|  
ACCAAGAAGGAGAACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTT 360  
Thr Lys Lys Glu Asn Cys Pro Tyr Ser Ile Leu Glu Ile Thr Ser Val Glu Ile Gly Val  
|  
GTTGCCGTCAAAGCCATTAACAGCAACTATTACTGCCATGAACAGAAGGGAAACTC 420  
Val Ala Val Lys Ala Ile Asn Ser Asn Tyr Tyr Leu Ala Met Asn Lys Lys Gly Lys Leu  
|  
TATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGA 480  
Tyr Gly Ser Lys Glu Phe Asn Asn Asp Cys Lys Leu Lys Glu Arg Ile Glu Glu Asn Gly  
|  
TACAATACCTATGCATCATTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTG 540  
Tyr Asn Thr Tyr Ala Ser Phe Asn Trp Gln His Asn Gly Arg Gln Met Tyr Val Ala Leu  
|  
AATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAACACCTCTGCTCAC 600  
Asn Gly Lys Gly Ala Pro Arg Arg Gly Gln Lys Thr Arg Arg Lys Asn Thr Ser Ala His  
|  
TTTCTTCCAATGGTGGTACACTCATAG 627  
Phe Leu Pro Met Val Val His Ser \*

FIG.23

ATGACCTGCCAGGCTCTGGGTCAAGGACATGGTTCTCCGAAGCTACCAACTCTTCCTCT 60  
MetThrCysG1nA1aLeuG1yG1nAspMetVa1SerProG1uA1aThrAsnSerSerSer  
  
TCCTCTTCTCTTCCCCGTCTCCGCTGGTCGTACGTTGTTACAACCACCTGCAG 120  
SerSerPheSerSerProSerSerA1aG1yArgHisVa1ArgSerTyrAsnHisLeuG1n  
  
GGTGACGTTGTTGGCGTAAACTGTTCTCTTACCAAATACTCCTGAAAATCGAAAAAA 180  
G1yAspVa1ArgTrpArgLysLeuPheSerPheThrLysTyrPheLeuLysI1eG1uLys  
  
AACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCATCCTGGAGATAACA 240  
AsnG1yLysVa1SerG1yThrLysLysG1uAsnCysProTyrSerI1eLeuG1uI1eThr  
  
TCAGTAGAAATCGGAGTTGTTGCCGTCAAAGCCATTAAACAGCAACTATTACTGCCATG 300  
SerVa1G1uI1eG1yVa1Va1A1aVa1LysA1aI1eAsnSerAsnTyrTyrLeuA1aMet  
  
ACAAGAAGGGGAAACTCTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAG 360  
AsnLysLysG1yLysLeuTyrG1ySerLysG1uPheAsnAsnAspCysLysLeuLysG1u  
  
AGGATAGAGGAAAATGGATACAATACCTATGCATCATTAACTGGCAGCATAATGGGAGG 420  
ArgI1eG1uG1uAsnG1yTyrAsnThrTyrA1aSerPheAsnTrpG1nHisAsnG1yArg  
  
CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG 480  
G1nMetTyrVa1A1aLeuAsnG1yLysG1yA1aProArgArgG1yG1nLysThrArgArg  
  
AAAAACACCTCTGCTCACTTCTCCAATGGTGGTACACTCATAG 525  
LysAsnThrSerA1aHisPheLeuProMetVa1Va1HisSer \*

FIG.24A

ATGACTTGCCAGGCACTGGGTCAAGACATGGTTCCCCGGAAGCTACCAACAGCTCCAGCTCTAGCTTCA  
70  
TACTGAACGGTCCGTGACCCAGTTCTGTACCAAAGGGCCTCGATGGTTGTCGAGGTGAGATCGAAGT  
M T C Q A L G Q D M V S P E A T N S S S S S F  
GCAGCCCACATCTAGCGCAGGTGTCACGTTCGCTCTTACAACCACTTACAGGGTGATGTTGTTGGCGCAA  
140  
CGTGGGTAGATCGCGTCCAGCAGTGCAAGCGAGAATGTTGGTGAATGTCCCACATAAGCAACCGCGTT  
S S P S S A G R H V R S Y N H L Q G D V R W R K  
ACTGTTCAGCTTACCAAGTACTTCCTGAAAATCGAAAAACGGTAAAGTTCTGGGACCAAGAAGGAG  
210  
TGACAAGTCGAAATGGTTCATGAAGGACTTTAGCTTTGCCATTCAAAGACCCCTGGTTCTTCCTC  
L F S F T K Y F L K I E K N G K V S G T K K E  
AACTGCCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCGTCAAAGCCATTAACA  
280  
TTGACGGGCATGTCGTAGGACCTCTATTGTAGTCATCTTAGCCTAACAAACGGCAGTTGGTAATTGT  
N C P Y S I L E I T S V E I G V V A V K A I N  
GCAACTATTACTTAGCCATGAACAAGAAGGGAAACTCTATGGCTAAAAGAATTAAACAATGACTGTAA  
350  
CGTTGATAATGAATCGGTACTTGTCTCCCTTGAGATACCGAGTTCTAAATTGTTACTGACATT  
S N Y Y L A M N K K G K L Y G S K E F N N D C K  
GCTGAAGGAGAGGATAGAGGAAAATGGATAACAATACCTATGCATCATTAACGGCAGCATAATGGGAGG  
420  
CGACTTCCTCTCCTATCTCCTTACCTATGTTATGGATAACGTAGTAAATTGACCGTGTATTACCCCTCC  
L K E R I E E N G Y N T Y A S F N W Q H N G R  
CAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAACACCT  
490  
GTTTACATAACCGTAACCTACCTTCTCGAGGTTCTCTCCTGTCTTTGTGCTTCCCTTGTGGA  
Q M Y V A L N G K G A P R R G Q K T R R K N T  
CTGCTCACTTTCTTCCAATGGTGGTACACTCATAG  
525  
GACGAGTGAAAGAAGGTTACCAACCATGTGAGTATC  
S A H F L P M V V H S

FIG.24B

ATGACCTGCCAGGCTCTGGGTCAAGGACATGGTTCTCCGGAAGCTACCAACTCTCC  
TCTTCCTCTTCTCTTCCCCGTCTCCGCTGGTCGTACGTTCTTACAACCAC  
CTGCAGGGTGACGTTGGCGTAAACTGTTCTCTTACCAAATACTTCCTGAAA  
ATCGAAAAAAACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATGGAGTTGCCGTAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACACAAGAAGGGAAACTCTATGGCTAAAAGAATTAAACAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAATGGATAACAATACCTATGCATCATT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTCTTCCAATGGT  
GTACACTCATAG

MTCQALGQDMVSPEATNSSSSSFSSPSSAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIE  
KNGVSGTKKENCPYSILEITSVEIGVVAVKAINSYYLAMNKKGKLGSKEFNNDCKL  
KERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.25

ATGGCTGGTCGTACGTTCTTACAACCACCTGCAGGGTGACGTTGGCGT  
AAACTGTTCTCTTACCAAATACTCCTGAAAATCGAAAAAAACGGTAAAGTTCT  
GGGACCAAGAAGGAGAACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGGCATTGAACAGCAACTATTACTAGCCATGAACAAGAAG  
GGGAAACTCTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATA  
GAGGAAAATGGATAACAATACCTATGCATCTTAACTGGCAGCATAATGGGAGGCAA  
ATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGG  
AAAAACACCTCTGCTCACTTCTTCCAATGGTGGTACACTCATAG

MAGRHVRSYNHLQGDVRWRKLFSFTKYFLKIEKNGVSGTKKENCPYSILEITSVEIGV  
VAVKAINSYYLAMNKKGKLGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVA  
LNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.26

ATGGTTGTTGGCGTAAACTGTTCTCTTACCAAATACTTCCTGAAAATCGAAAAA  
AACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCATCCTGGAGATA  
ACATCAGTAGAAATCGGAGTTGTTGCCGTAAAGCCATTAACAGCAACTATTACTTA  
GCCATGAACAAGAAGGGGAAACTCTATGGCTAAAAGAATTAAACAATGACTGTAAG  
CTGAAGGAGAGGATAGAGGAAAATGGATAACAATACCTATGCATCATTAACTGGCAG  
CATAAATGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGA  
CAGAAAACACGAAGGAAAAACACCTCTGCTCACTTCTTCCAATGGTGGTACACTCA  
TAG

MVRWRKLFSFTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSYYLAM  
NKKGKL YGSKEFNNDCKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTR  
RKNTSAHFLPMVVHS.

## FIG.27

ATGGAAAAAAACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCAT  
CCTGGAGATAACATCAGTAGAAATCGGAGTTGTTGCCGTAAAGCCATTAACAGCA  
ACTATTACTTAGCCATGAACAAGAAGGGGAAACTCTATGGCTAAAAGAATTAAAC  
AATGACTGTAAGCTGAAGGAGAGGATAGAGGAAAATGGATAACAATACCTATGCATC  
ATTTAACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAG  
CTCCAAGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTCTTCCA  
ATGGTGGTACACTCATAG

MEKNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSYYLAMNKKGKL YGSKEFNNDC  
KLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVH  
S.

## FIG.28

ATGGAGAACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATCGGAGTTGT  
TGCCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAAC  
TCTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA  
AATGGATACAATACCTATGCATCATTAACTGGCAGCATAATGGGAGGCAAATGTA  
TGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAA  
ACACCTCTGCTCACTTCTCCAATGGTGGTACACTCATAG

MENCPSILEITSVEIGVVAVKAINSYYLAMNKKKL YGSKEFNNNDKLKERIEENGY  
NTYASFNWQHNGRQMYVALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.29

ATGGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAGGGGAAACT  
CTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAGGATAGAGGAA  
ATGGATACAATACCTATGCATCATTAACTGGCAGCATAATGGGAGGCAAATGTAT  
GTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACACGAAGGAAAAAA  
CACCTCTGCTCACTTCTCCAATGGTGGTACACTCATAG

MVKAINSYYLAMNKKKL YGSKEFNNNDKLKERIEENGYNTYASFNWQHNGRQMY  
VALNGKGAPRRGQKTRRKNTSAHFLPMVVHS.

## FIG.30

ATGGGGAACTCTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAGGAGAG  
GATAGAGGAAAATGGATAACAATACCTATGCATCATTAACTGGCAGCATAATGGGA  
GGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCAAGGAGAGGACAGAAAACA  
CGAAGGAAAACACCTCTGCTCACTTCTCCAATGGTGGTACACTCATAG

MGKL YGSKEFNNNDKLKERIEENGYNTYASFNWQHNGRQMYVALNGKGAPRRGQKT  
RRRKNTSAHFLPMVVHS.

## FIG.31

ATGACCTGCCAGGCTCTGGTCAGGACATGGTTCTCCGGAAGCTACCAACTCTTCC  
TCTTCCTCTTCTCTTCCCCGTCTCCGCTGGTCGTACGTTCTTACAACCCAC  
CTGCAGGGTGACGTTCGTGGCGTAAACTGTTCTCTTACCAAATACTTCTGAAA  
ATCGAAAAAAACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTCGCGTCAAAGCCATTAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGAAACTCTATGGCTAAAAGAATTAAACAAT  
GACTGTAAGCTGAAG

MTCQALGQDMVSPEATNSSSSFSSPSSAGRHVR\$YNHLQGDVRWRKLF\$FTKYFLKIE  
KNGKVSGTKKENCPYSILEITSVEIGVVAVKAINSYYLAMNKKGKL YGSKEFNNDCKL  
K

## FIG.32

ATGGCTGGTCGTACGTTCTTACAACCACCTGCAGGGTGACGTTGGCGT  
AAACTGTTCTCTTACCAAATACTTCTGAAAATCGAAAAAAACGGTAAAGTTCT  
GGGACCAAGAAGGAGAACTGCCGTACAGCATCCTGGAGATAACATCAGTAGAAATC  
GGAGTTGTCGCGTCAAAGCCATTAACAGCAACTATTACTTAGCCATGAACAAGAAG  
GGGAAACTCTATGGCTAAAAGAATTAAACAATGACTGTAAGCTGAAG

MAGRHVR\$YNHLQGDVRWRKLF\$FTKYFLKIEKNGKVSGTKKENCPYSILEITSVEIGV  
VAVKAINSYYLAMNKKGKL YGSKEFNNDCKLK

## FIG.33

C-37 To Ser

ATGACCTCTCAGGCTCTGGTCAGGACATGGTTCTCCGAAGCTACCAACTCTCC  
TCTTCCTCTTCTCTCCCCGTCTCCGCTGGTCGTACGTTCTTACAACCAC  
CTGCAGGGTGACGTTGGCGTAAACTGTTCTTACCAAATACTTCCTGAAA  
ATCGAAAAAAACGGTAAAGTTCTGGGACCAAGAAGGAGAACTGCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGAAACTCTATGGCTAAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAATGGATACAATACCTATGCATCATT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTCTTCCAATGGTG  
GTACACTCATAG

**FIG.34**

C-106 To Ser

ATGACCTGCCAGGCTCTGGTCAGGACATGGTTCTCCGAAGCTACCAACTCTCC  
TCTTCCTCTTCTCTCCCCGTCTCCGCTGGTCGTACGTTCTTACAACCAC  
CTGCAGGGTGACGTTGGCGTAAACTGTTCTTACCAAATACTTCCTGAAA  
ATCGAAAAAAACGGTAAAGTTCTGGGACCAAGAAGGAGAACTCTCCGTACAGCATC  
CTGGAGATAACATCAGTAGAAATCGGAGTTGTCGTCAAAGCCATTAAACAGCAAC  
TATTACTTAGCCATGAACAAGAAGGGAAACTCTATGGCTAAAAGAATTAAACAAT  
GACTGTAAGCTGAAGGAGAGGATAGAGGAAATGGATACAATACCTATGCATCATT  
AACTGGCAGCATAATGGGAGGCAAATGTATGTGGCATTGAATGGAAAAGGAGCTCCA  
AGGAGAGGACAGAAAACACGAAGGAAAAACACCTCTGCTCACTTCTTCCAATGGTG  
GTACACTCATAG

**FIG.35**

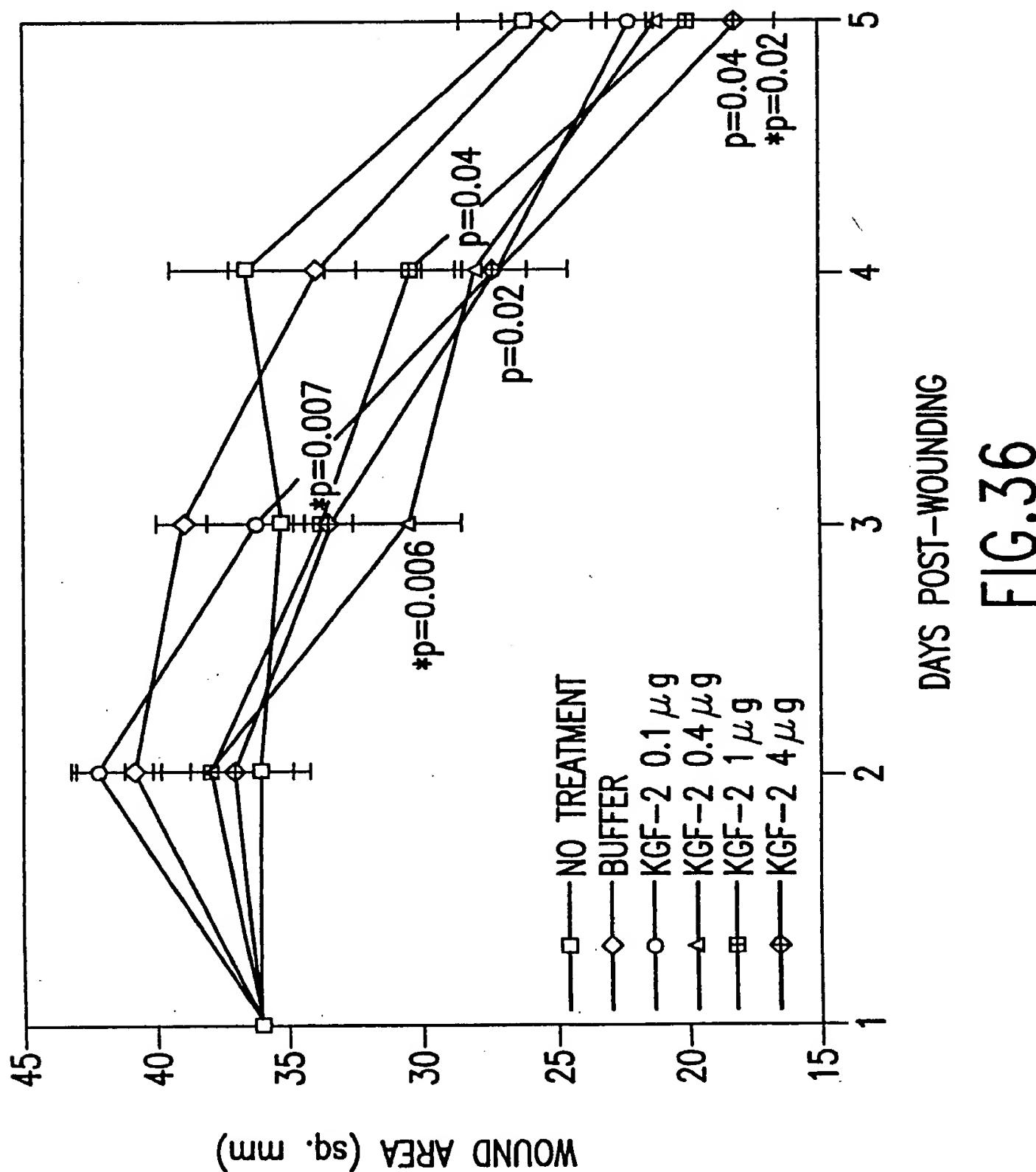


FIG. 36

EFFECT OF KGF-2  $\Delta$ 33 ON NORMAL WOUND HEALING RAT MODEL

TREATMENT GROUPS	WOUND SIZE (mm)	% WOUND CLOSURE	HISTOLOGICAL SCORE	RE-EPITH. ( $\mu$ m)	BrdU SCORE
NO TREATMENT	25.9 $\pm$ 2.5	58.8 $\pm$ 3.7	6.8 $\pm$ 0.2	1142 $\pm$ 141	3.8 $\pm$ 0.4
BUFFER	25.1 $\pm$ 1.7	60.2 $\pm$ 2.6	6.4 $\pm$ 0.2	923 $\pm$ 61	5.0 $\pm$ 0.4
KGF-2/ $\Delta$ 33 (0.1 $\mu$ g)	22.0 $\pm$ 0.9	65 $\pm$ 1.4	6.8 $\pm$ 0.2	1275 $\pm$ 148	4.6 $\pm$ 0.7
KGF-2/ $\Delta$ 33 (0.4 $\mu$ g)	21.1 $\pm$ 1.4	68.4 $\pm$ 2.4	8.0 $\pm$ 0.5 p=0.0445*	1310 $\pm$ 182	4.2 $\pm$ 0.7
KGF-2/ $\Delta$ 33 (1.0 $\mu$ g)	19.9 $\pm$ 1.5	66.2 $\pm$ 2.1	8.4 $\pm$ 0.4 p=0.0159* p=0.0053†	1389 $\pm$ 115 p=0.0074†	3.3 $\pm$ 0.25 p=0.0217†
KGF-2/ $\Delta$ 33 (4.0 $\mu$ g)	18.1 $\pm$ 1.6 p=0.0398*	71.2 $\pm$ 2.6 p=0.0367*	8.5 $\pm$ 0.3 p=0.0047*	1220 $\pm$ 89 p=0.0200† p=0.0217†	5.3 $\pm$ 0.9 p=0.0254† p=0.0445†

FIG. 37

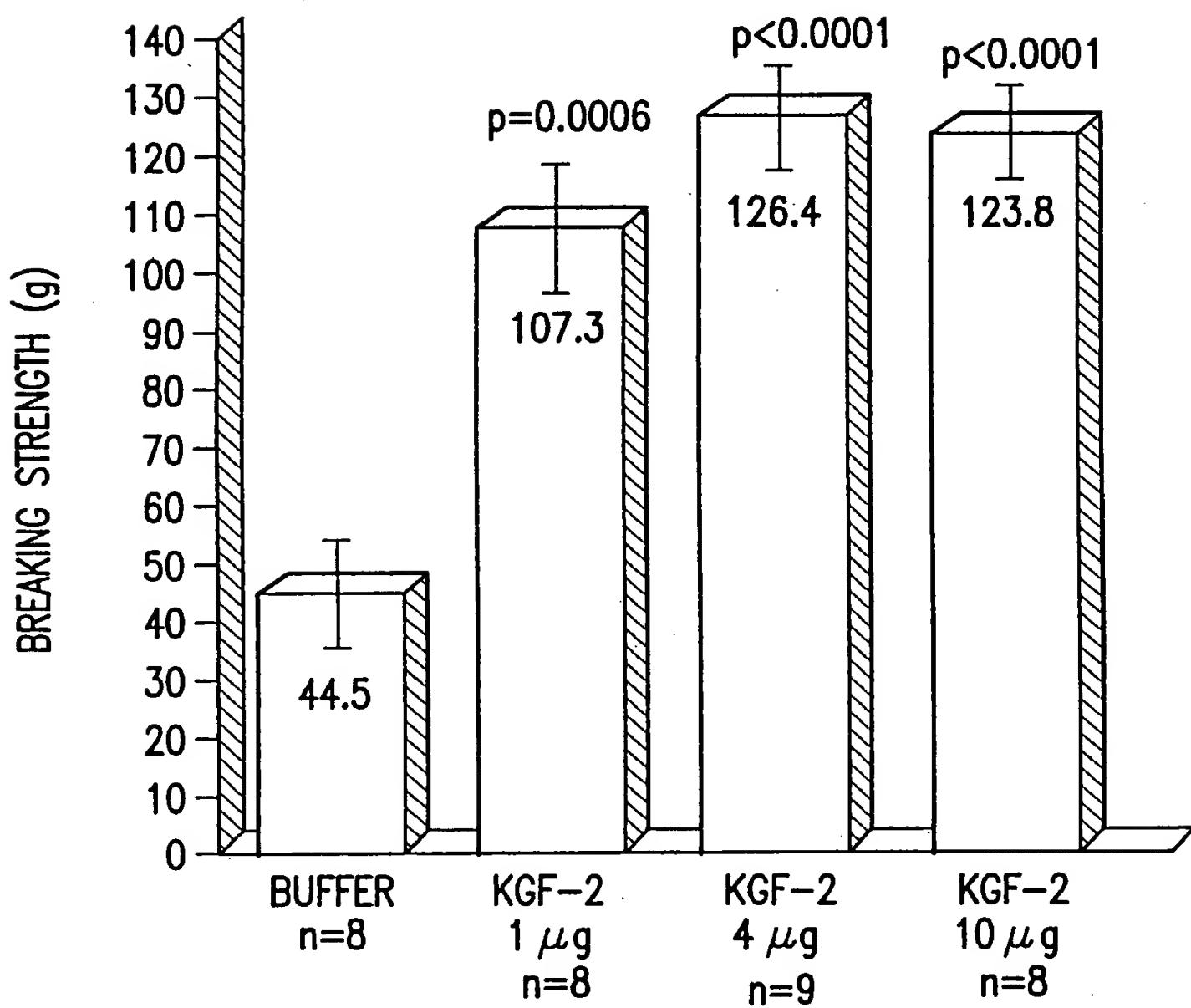


FIG.38

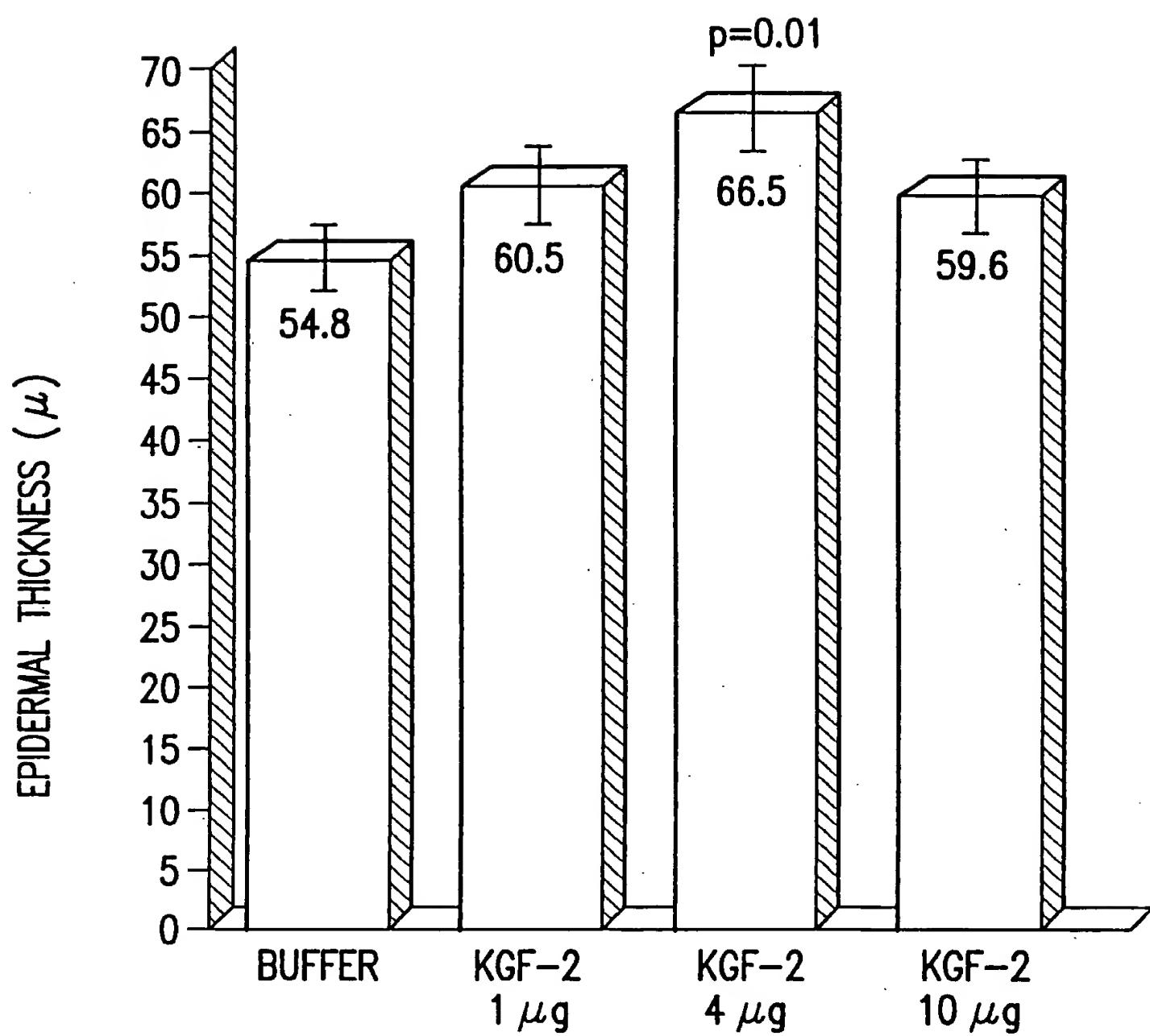


FIG.39

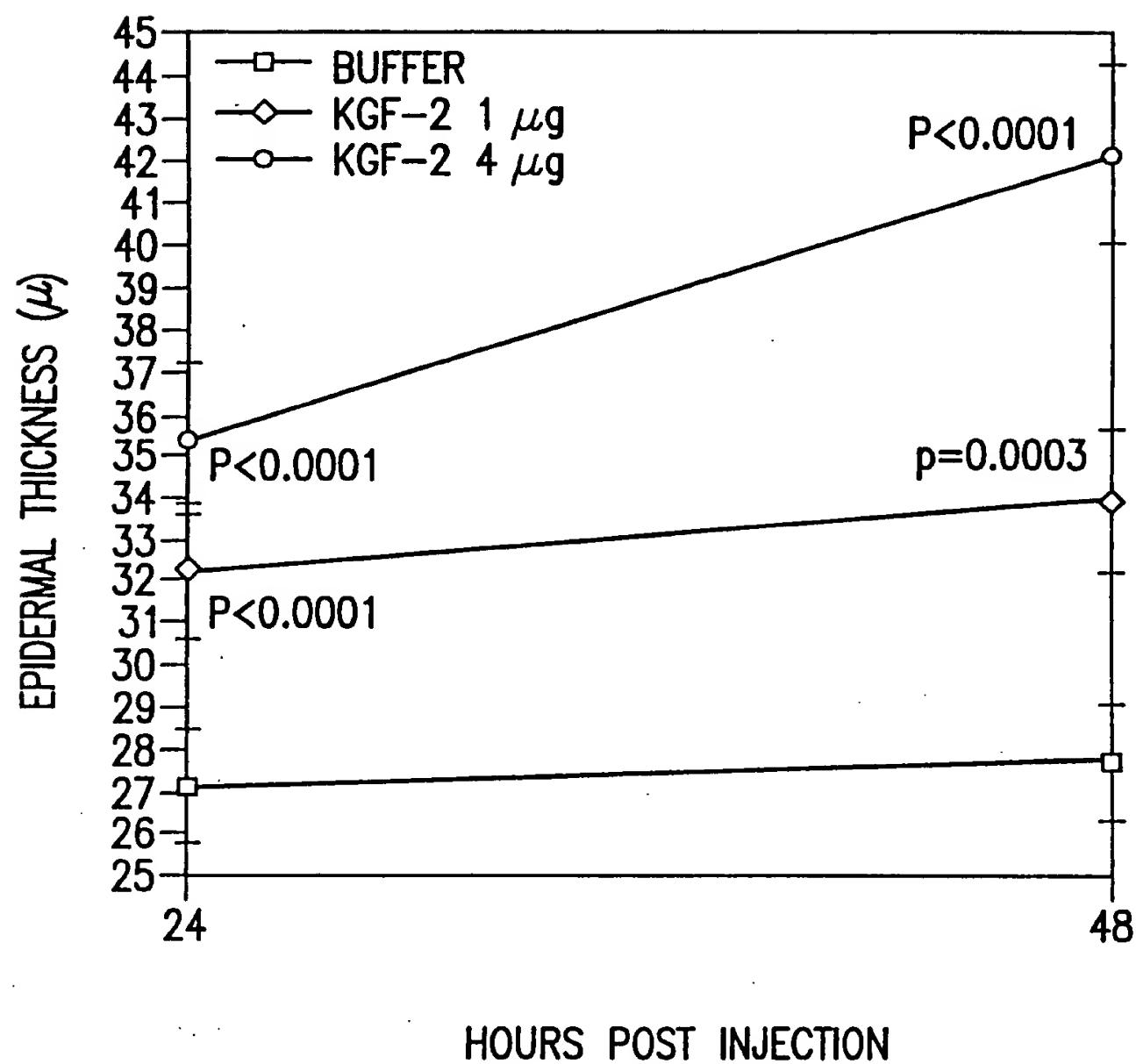


FIG. 40

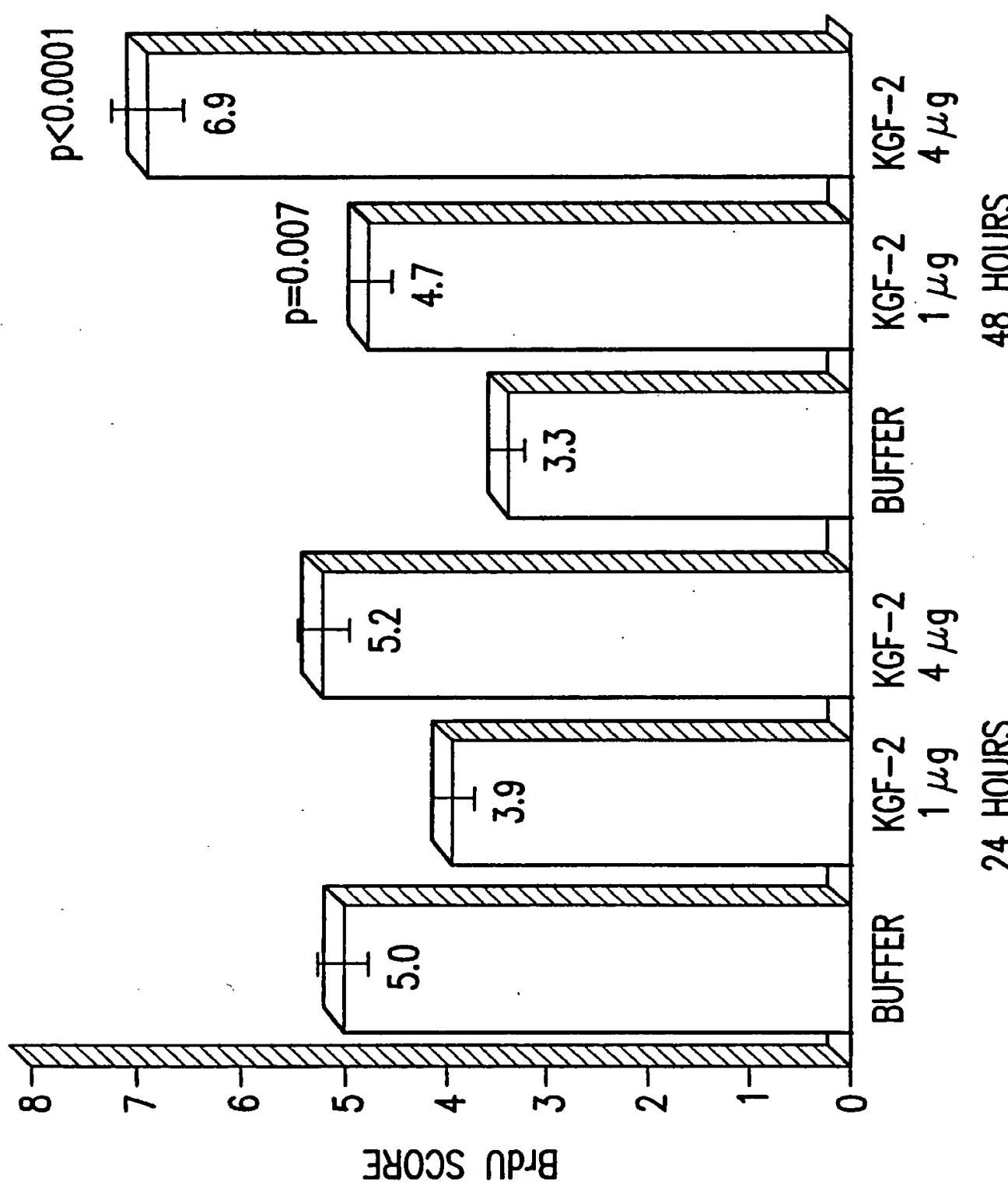


FIG. 41

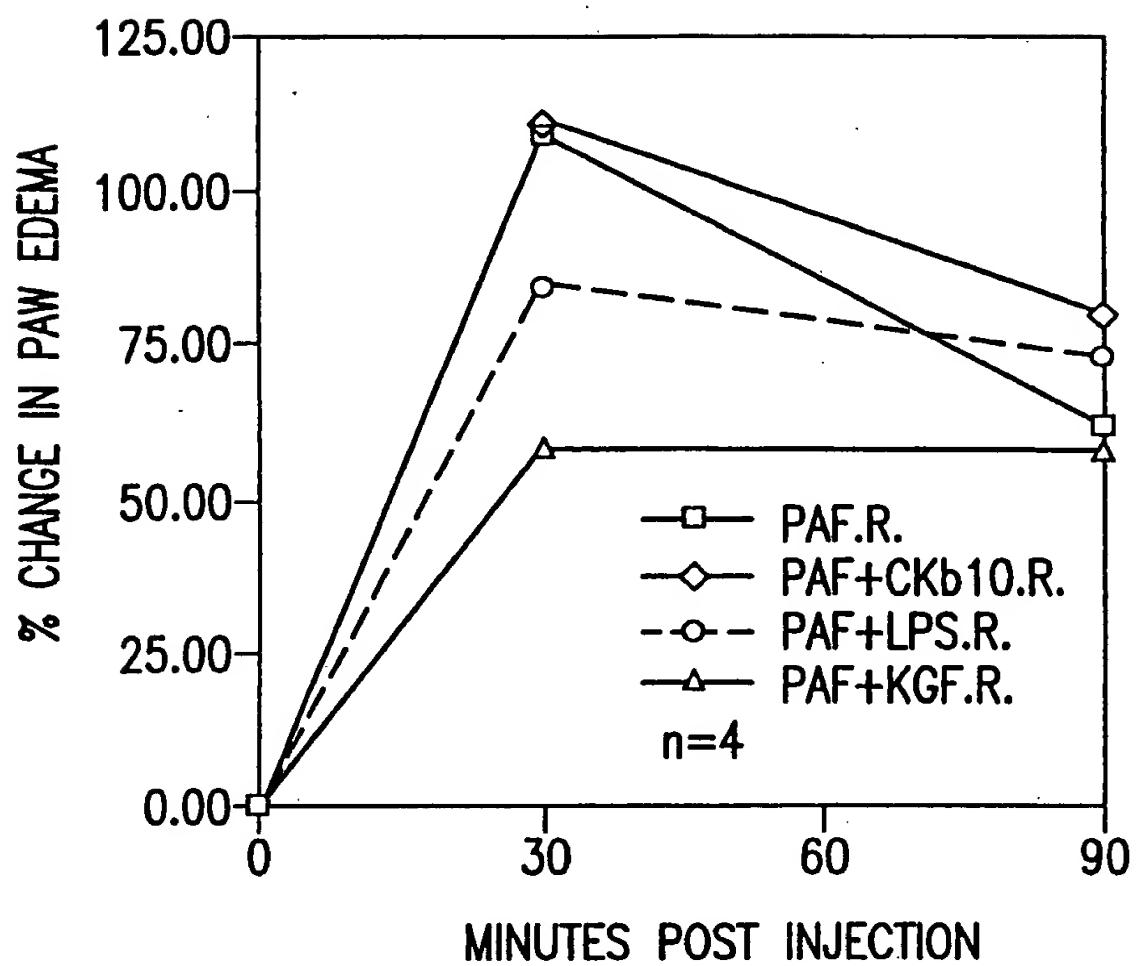


FIG.42A

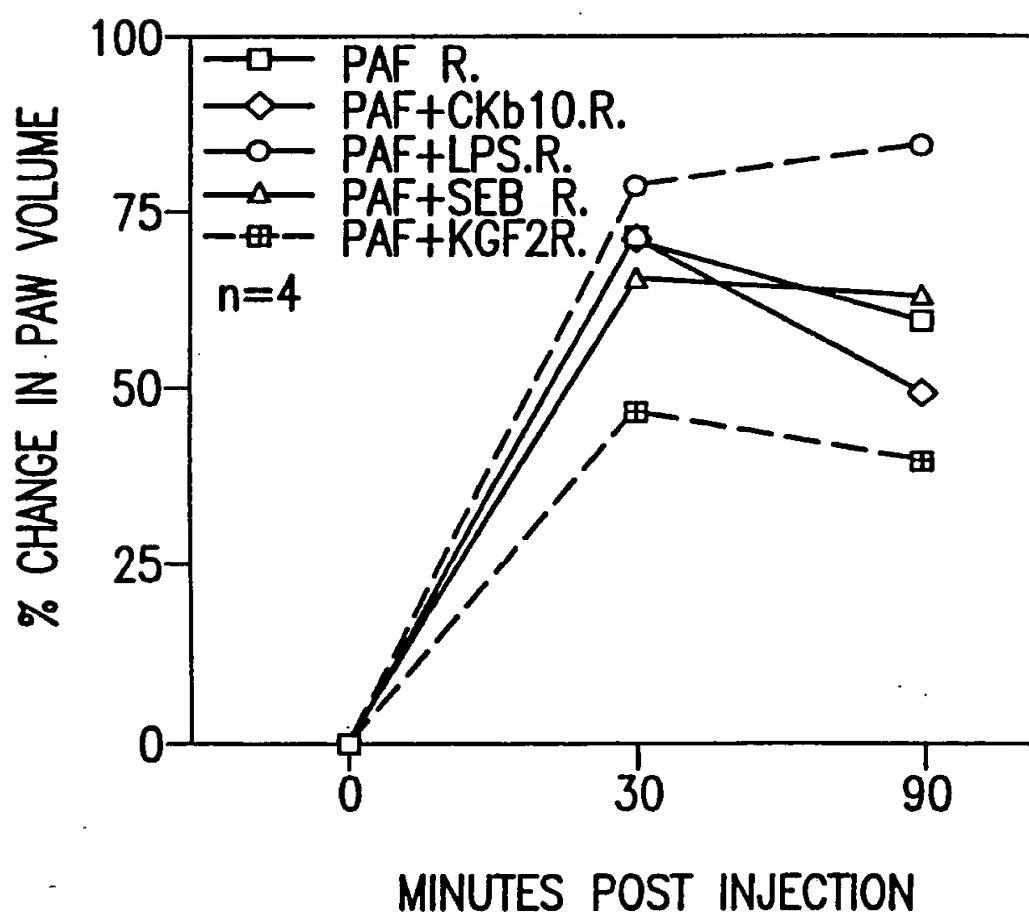


FIG.42B

EFFECT OF KGF-2  $\Delta$ 33 ON PAF-INDUCED PAW EDEMA IN LEWIS RATS

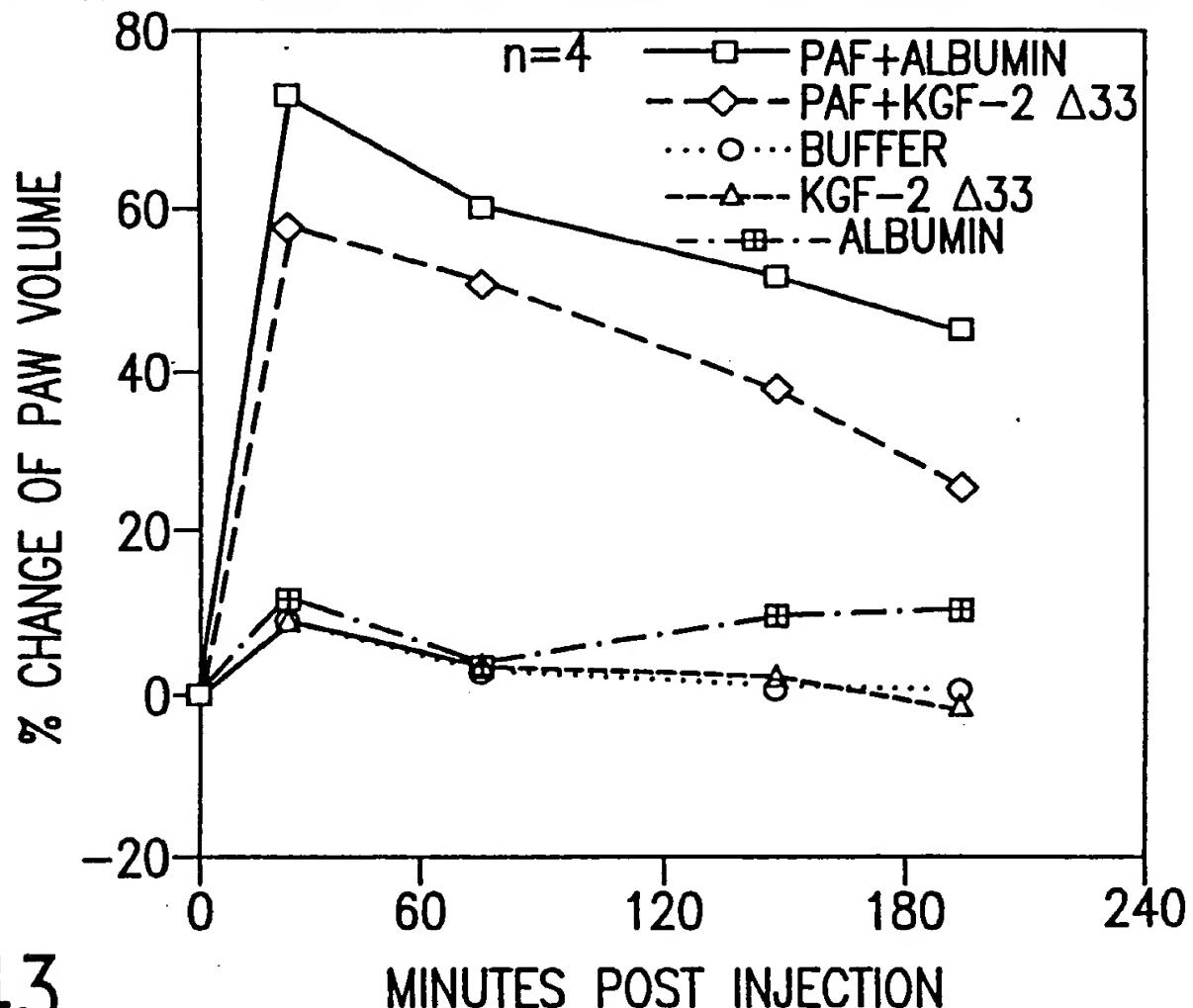


FIG.43

EFFECT OF KGF-2  $\Delta$ 33 ON SURVIVAL OF WHOLE BODY IRRADIATED Balb/c MICE

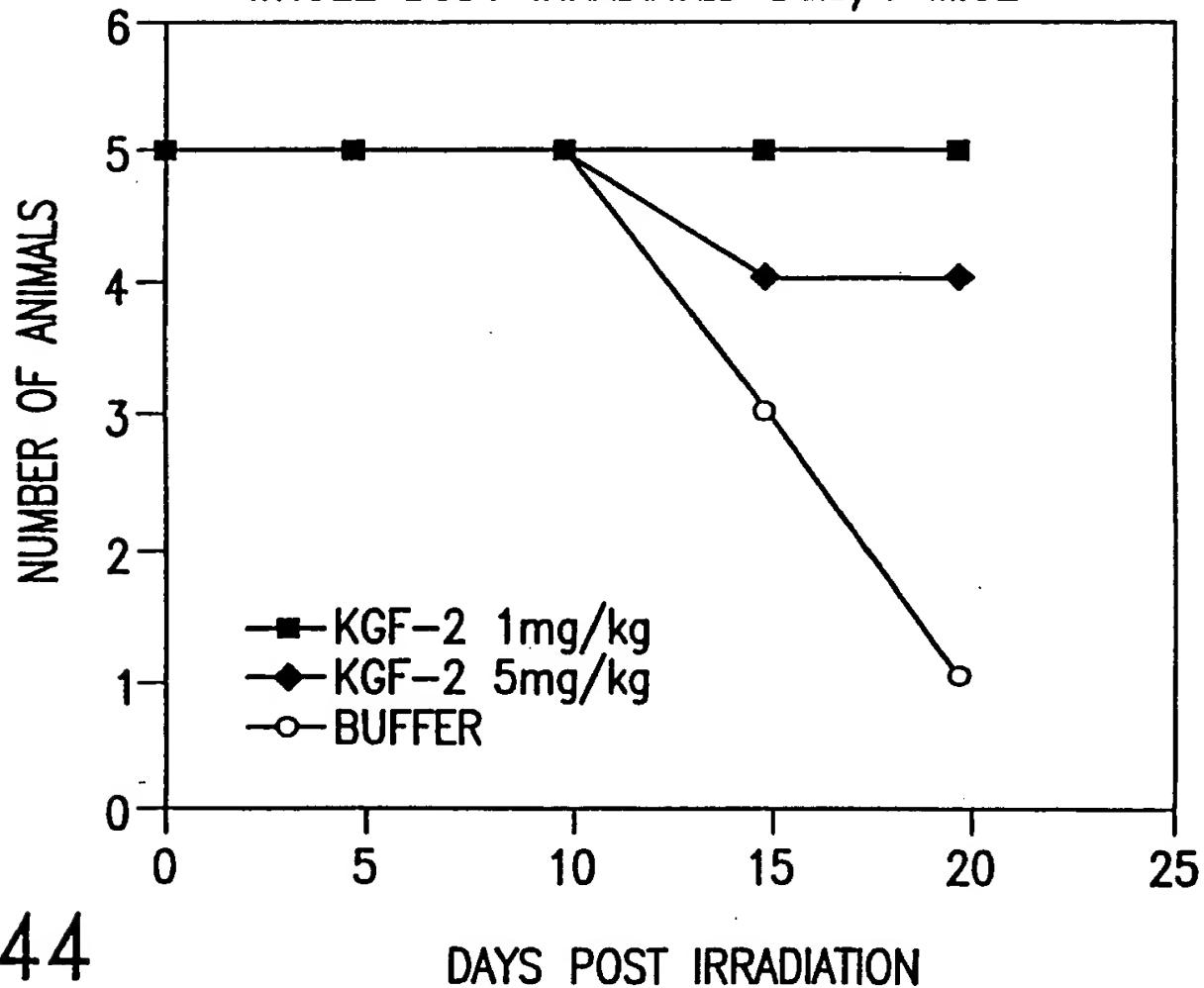


FIG.44

EFFECT OF KGF-2  $\Delta$ 33 ON BODY WEIGHT OF  
IRRADIATED MICE

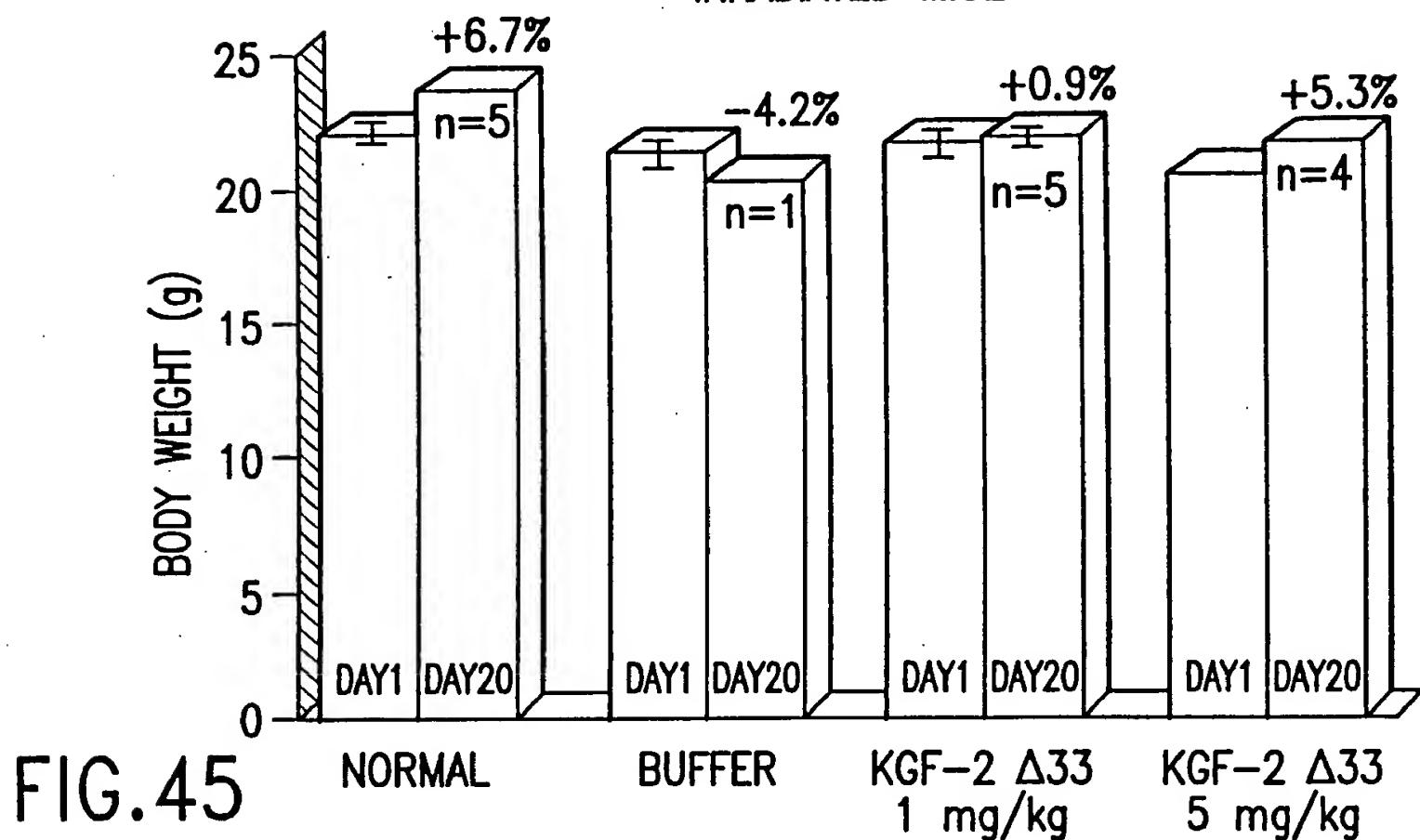


FIG. 45

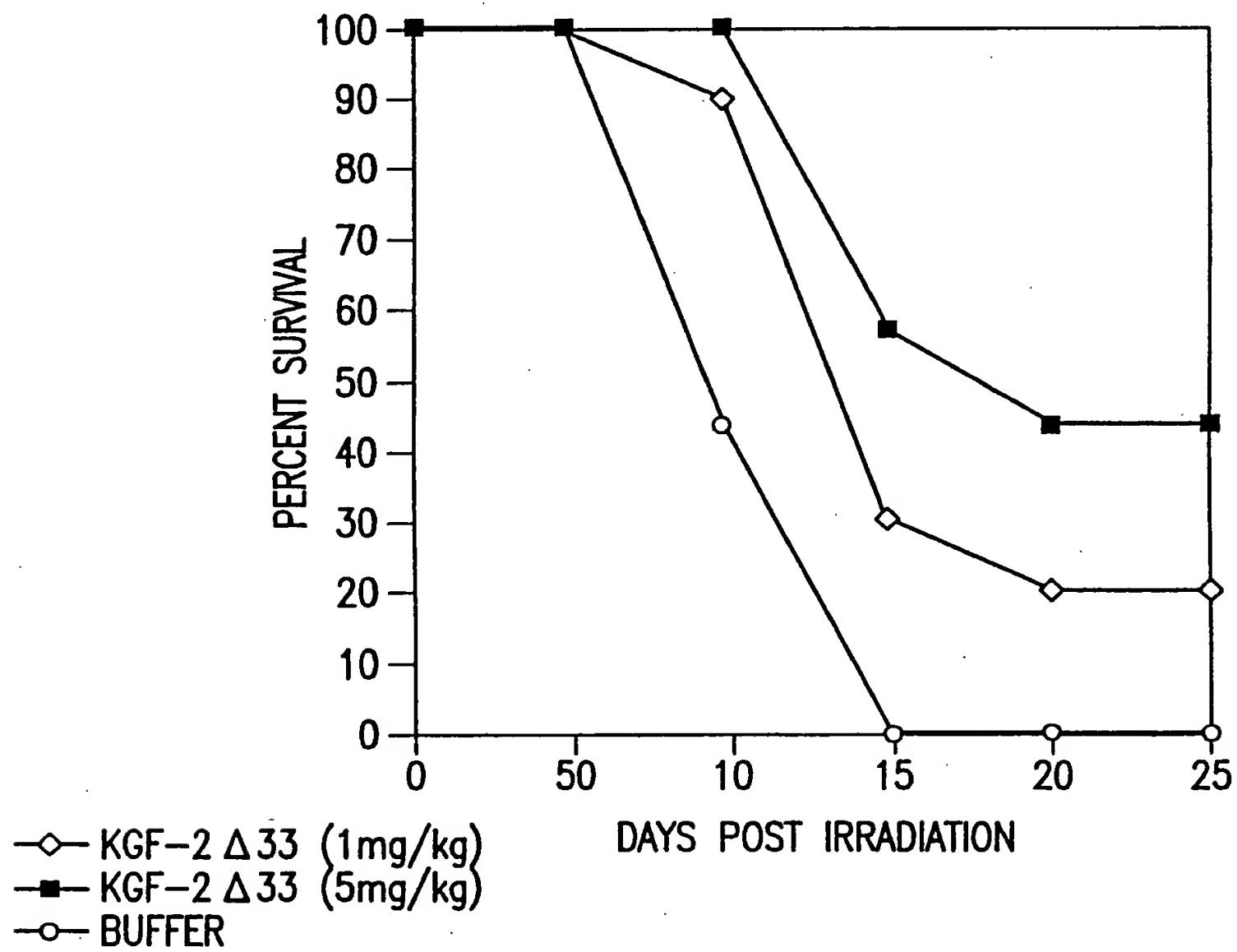


FIG. 46

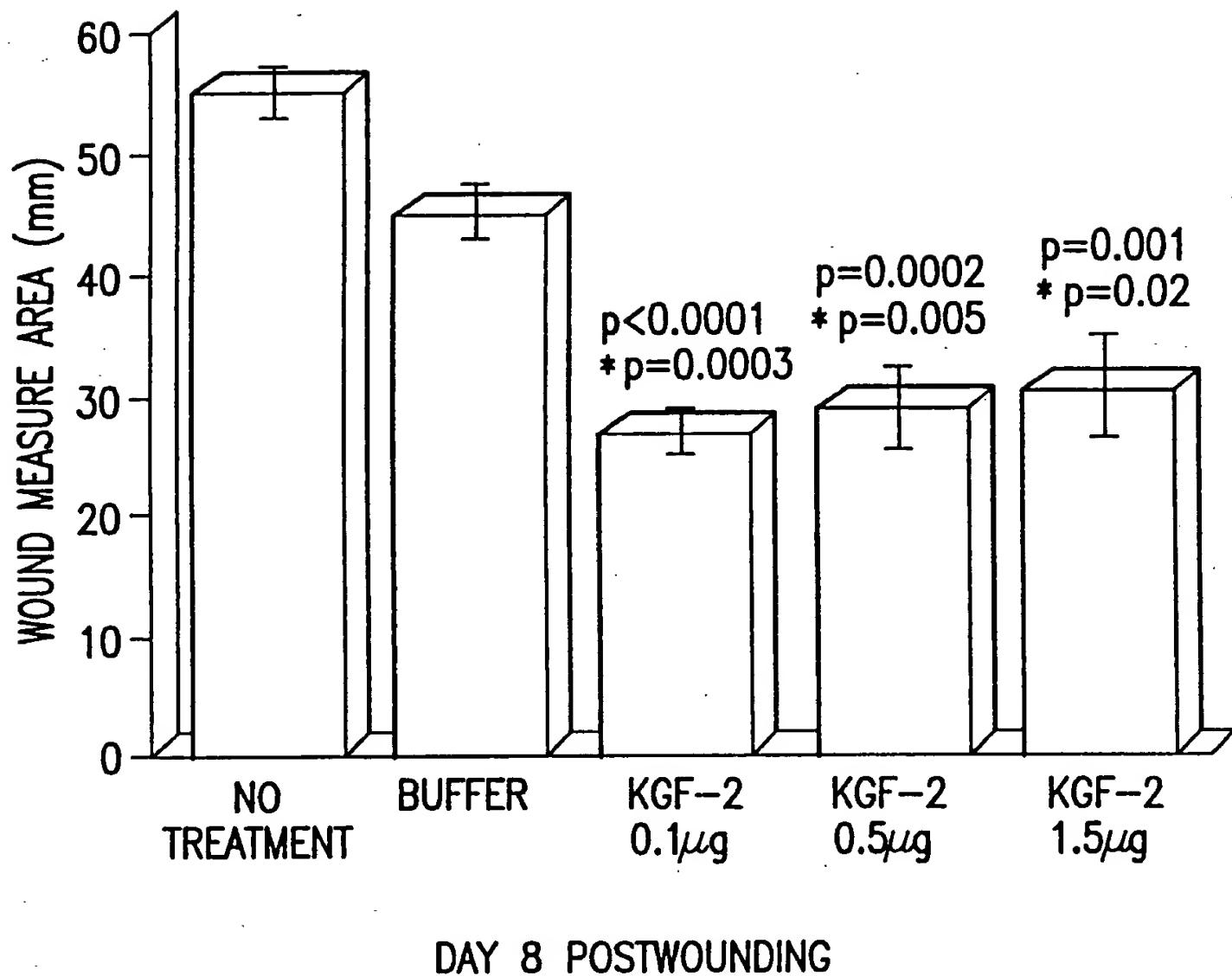


FIG.47

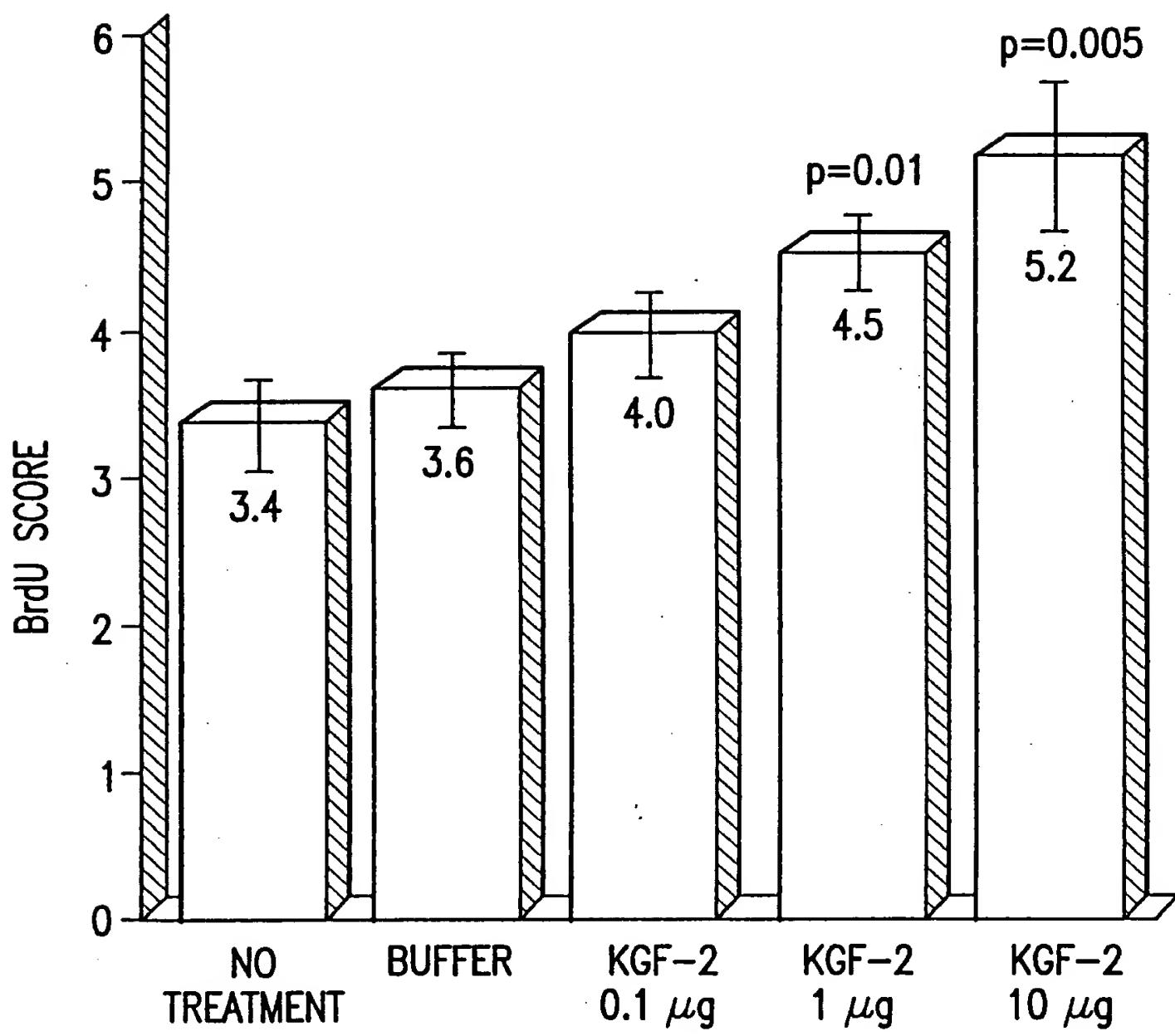


FIG. 48

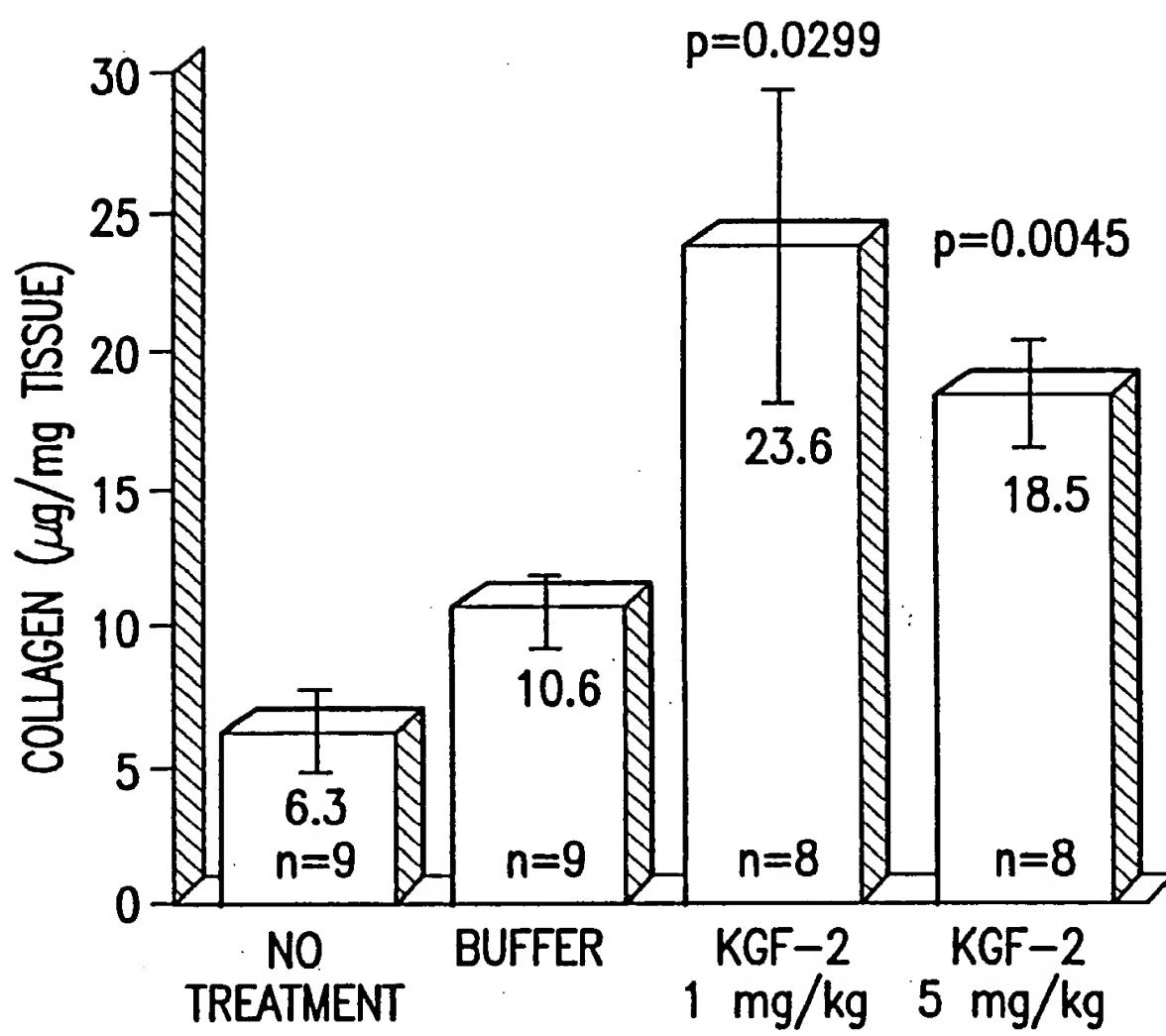


FIG. 49

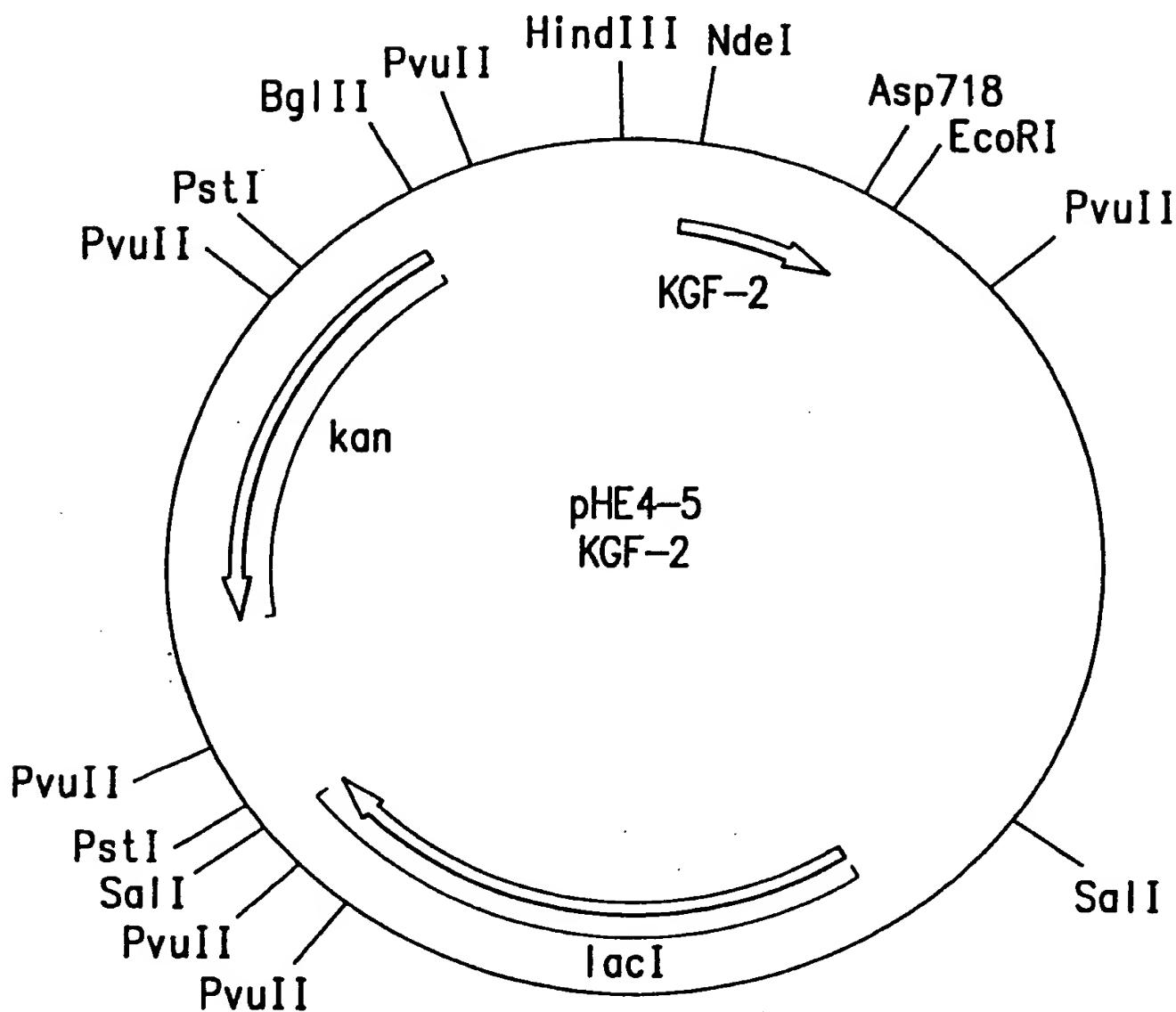


FIG. 50

1      AAGCTTAAAAAACTGCAAAAAATAGT **-35      Operator 1**  
      TTGACT **(TGTGAGCCGATAACAAT)**

50     **-10      Operator 2**  
      TAAGATGTACCCAATTGTGAGCCGATAACAATTTCACACATTAA

94     **S/D**  
      AGAGGGAGAAATTA    CATATG

FIG. 51

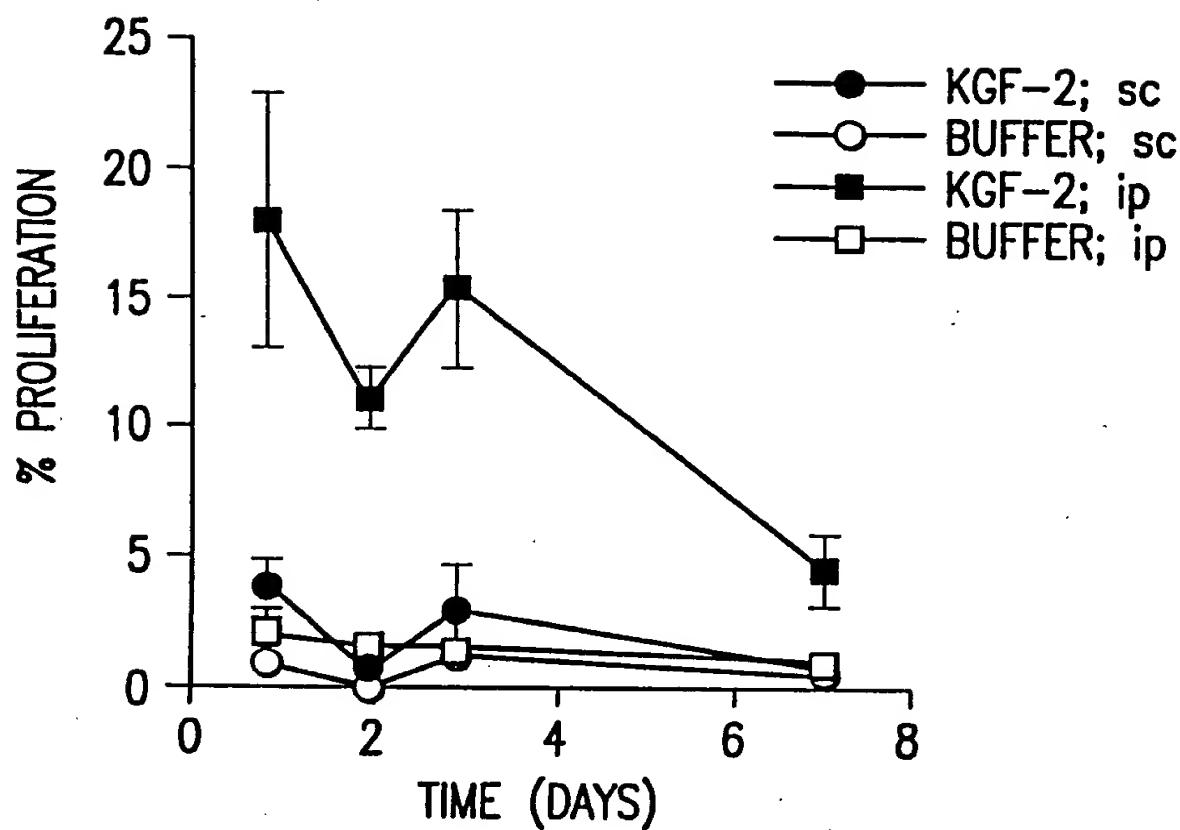


FIG. 52

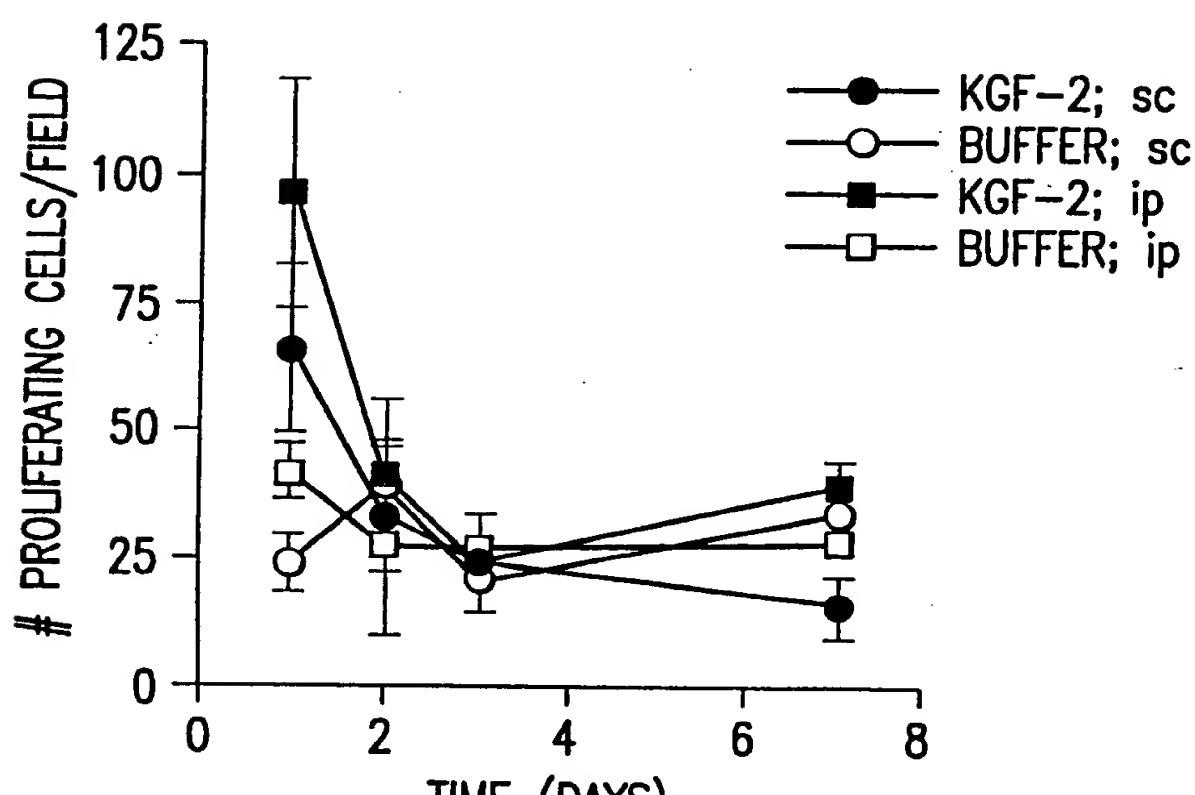


FIG. 53

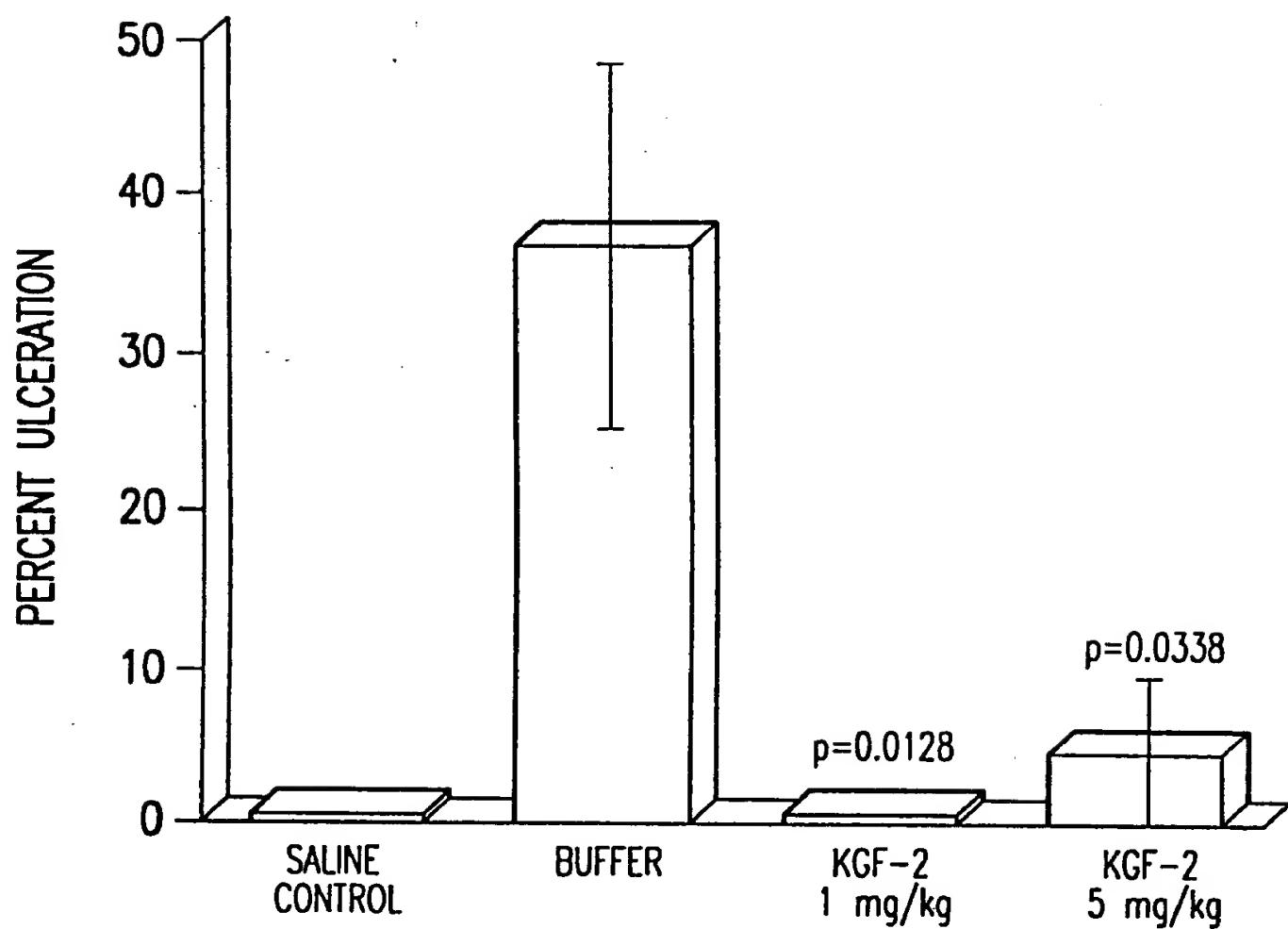


FIG. 54

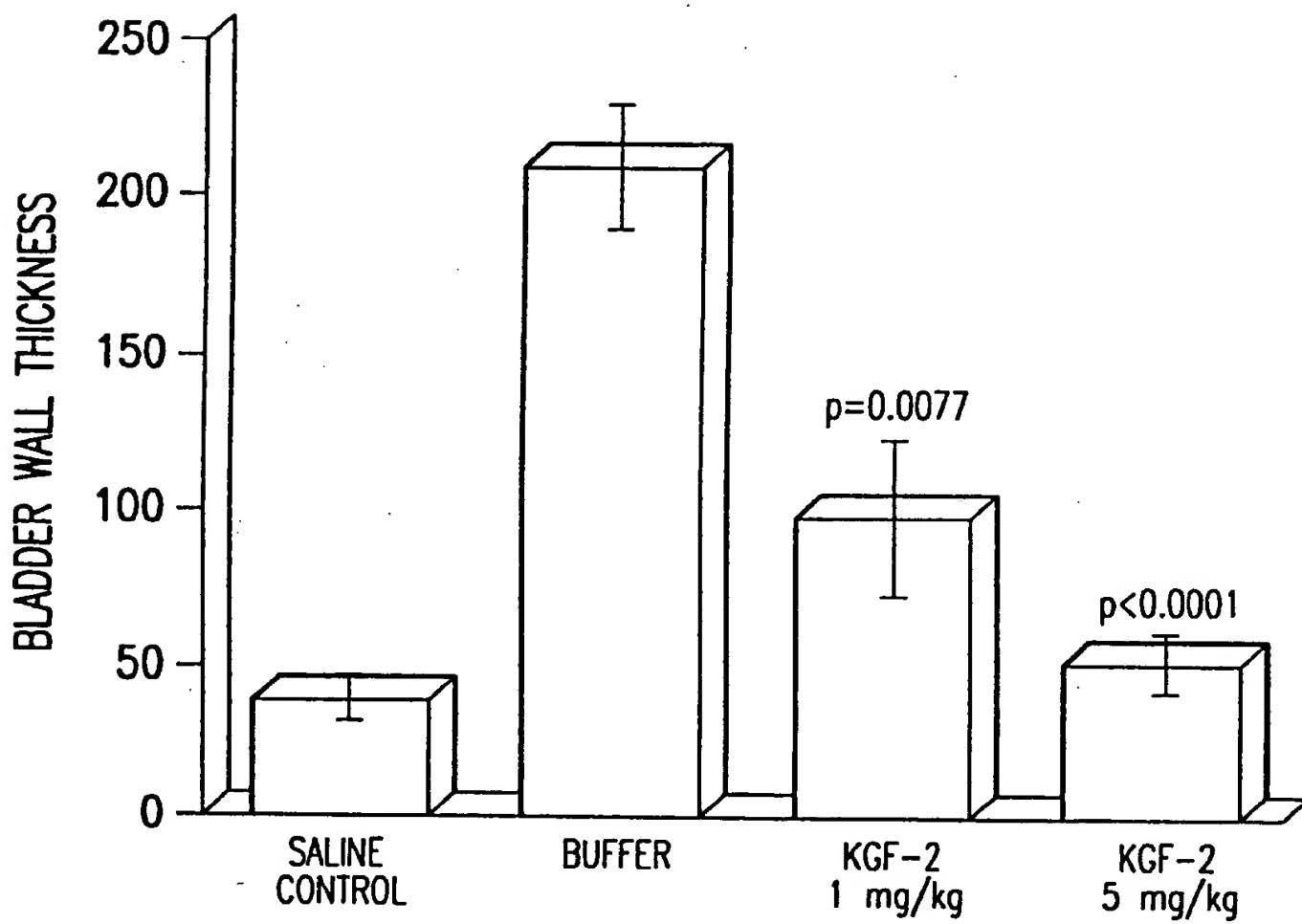


FIG. 55

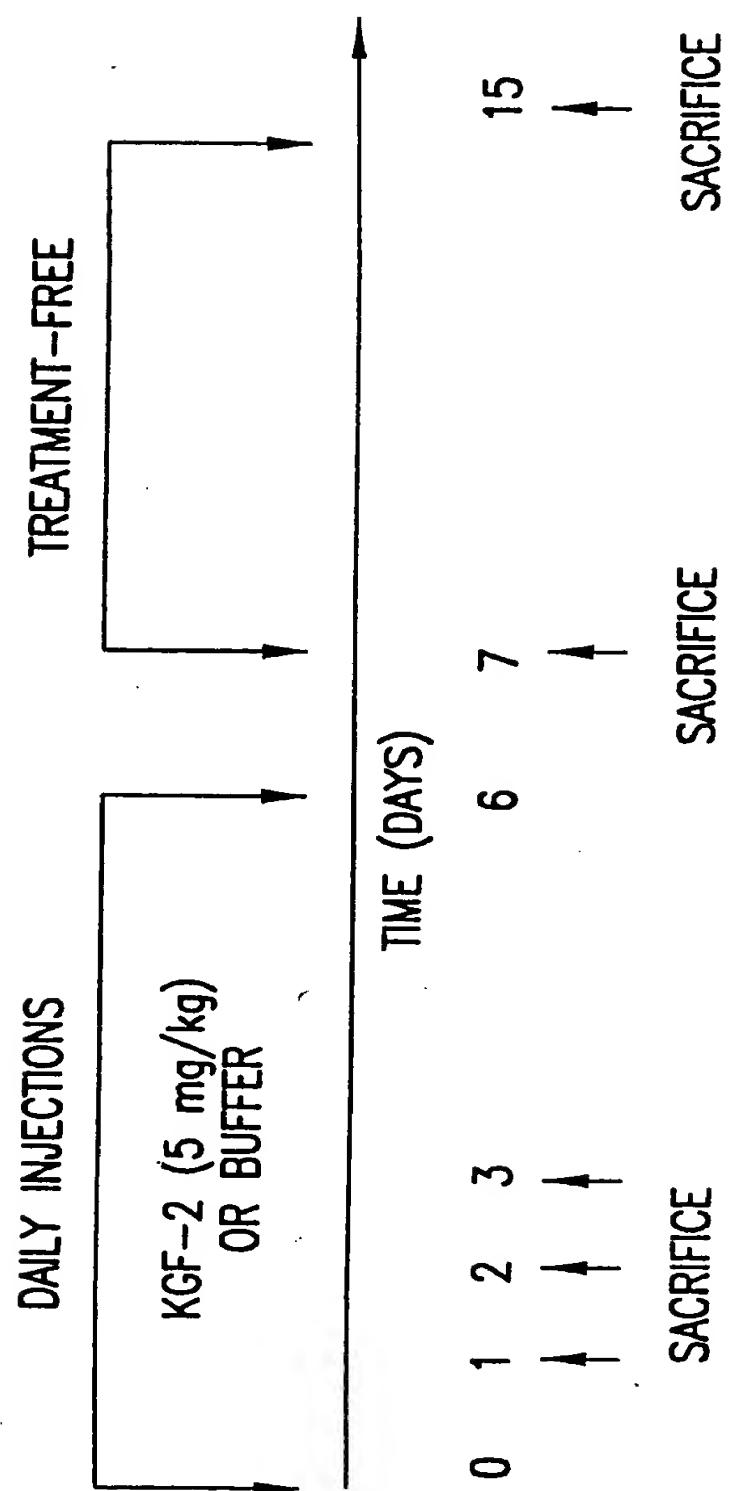


FIG. 56

PROLIFERATION OF HEPATOCYTES FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

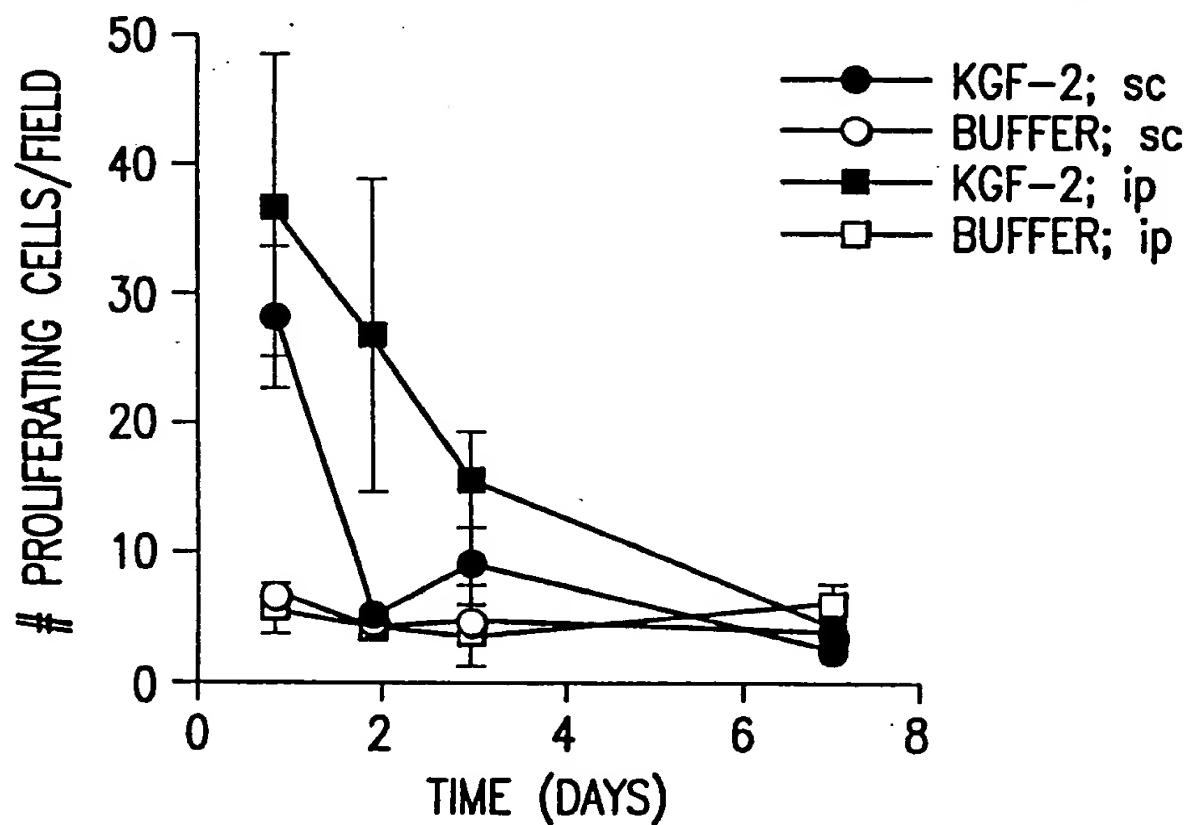


FIG. 57

PROLIFERATION OF PANCREATIC CELLS FOLLOWING SYSTEMIC ADMINISTRATION OF KGF-2

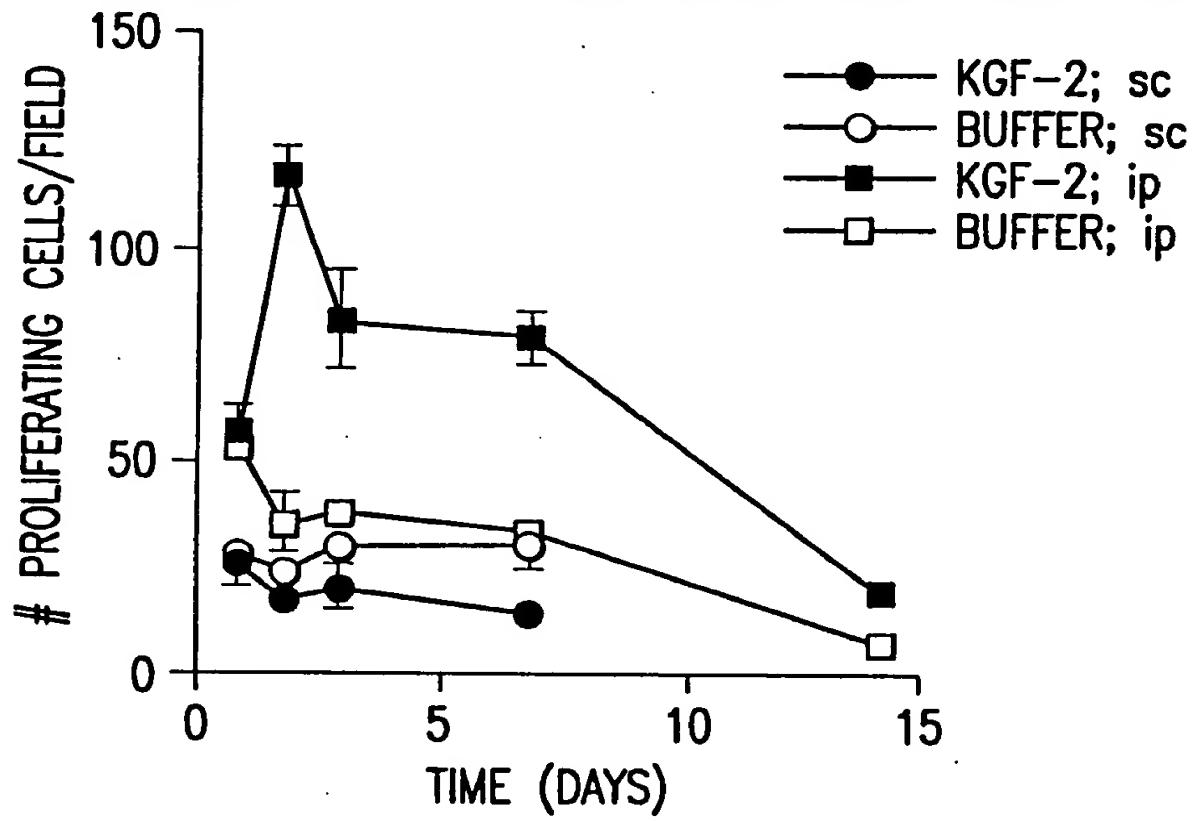


FIG. 58

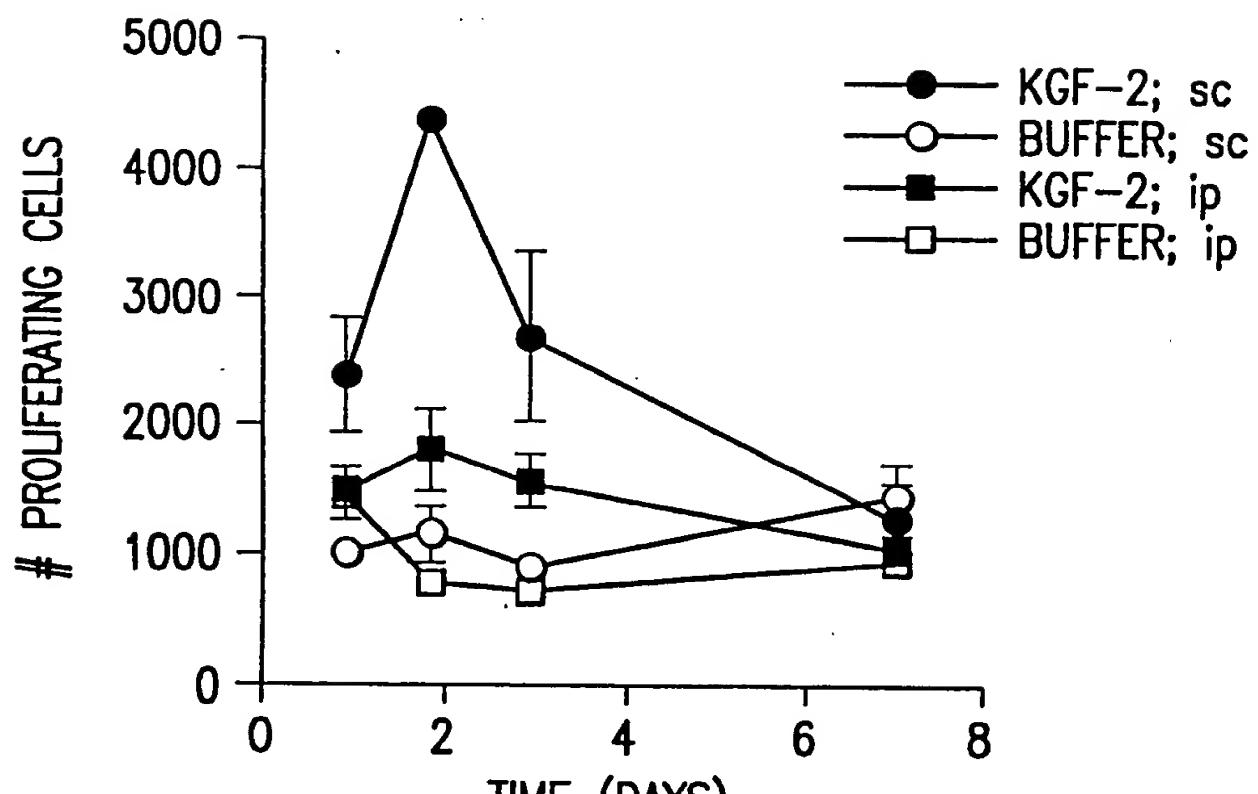


FIG. 59

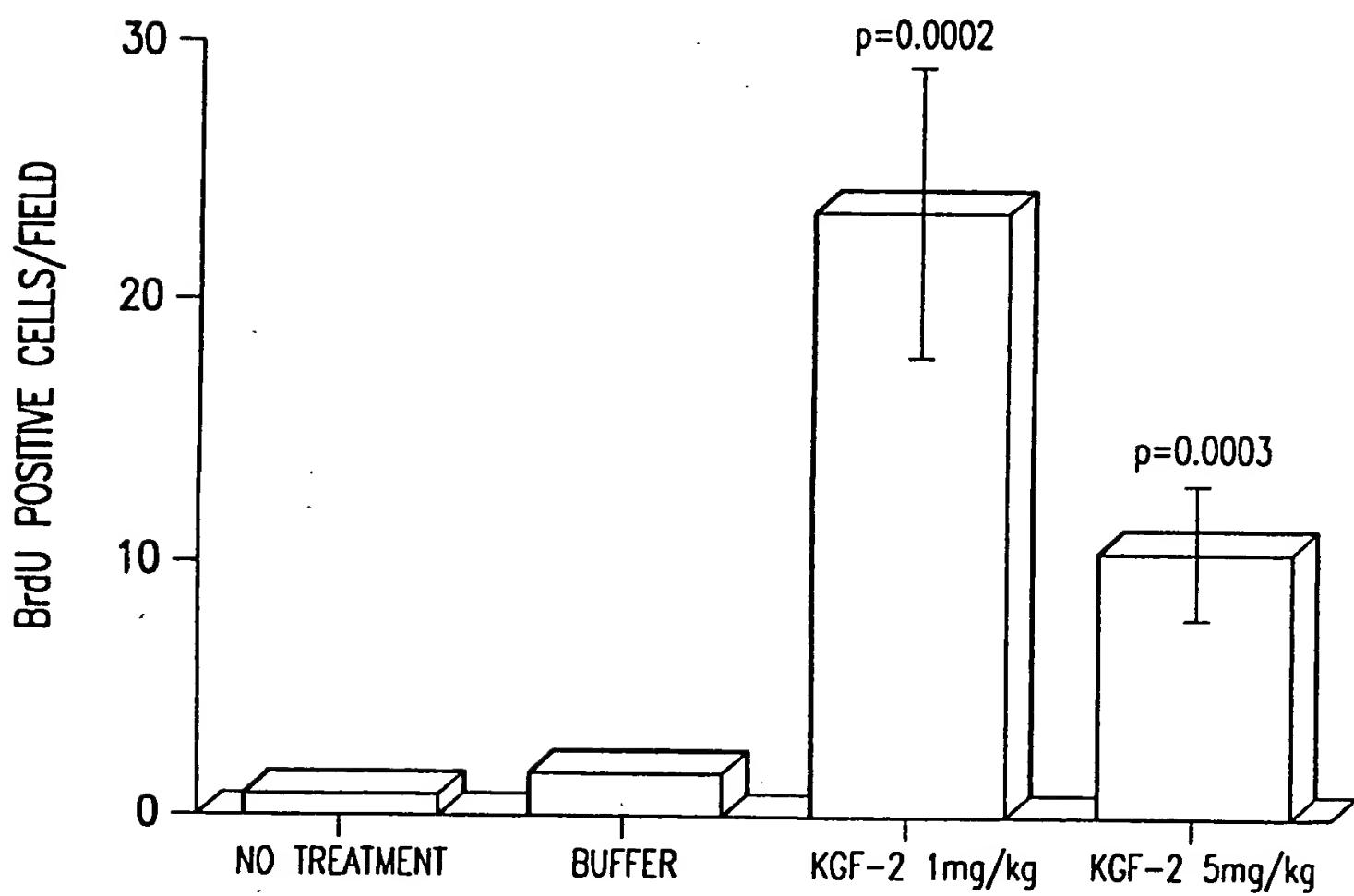


FIG. 60

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

**BLACK BORDERS**

**IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**

**FADED TEXT OR DRAWING**

**BLURRED OR ILLEGIBLE TEXT OR DRAWING**

**SKEWED/SLANTED IMAGES**

**COLOR OR BLACK AND WHITE PHOTOGRAPHS**

**GRAY SCALE DOCUMENTS**

**LINES OR MARKS ON ORIGINAL DOCUMENT**

**REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**

**OTHER: \_\_\_\_\_**

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**